

GenCore version 5.1.4_p5_4578
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UM nucleic - nucleic search, using sw model

Run on: March 17, 2003, 18:53:06 : Search time 1474 Seconds

(without alignments)
2593.036 Million cell updates/sec

Title: US-09-247-874C-2_COPY_8710_8945

Perfect score: 236

Sequence: 1 ttgtgctatctgtctaat.....ataactctactgaataaa 236

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum hit seq length: 0

Maximum hit seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: em_estdb:*
2: em_estdb:*
3: em_estdb:*
4: em_estdb:*
5: em_estdb:*
6: em_estdb:*
7: em_estdb:*
8: em_estdb:*
9: em_estdb:*
10: em_estdb:*
11: em_estdb:*
12: em_estdb:*
13: em_estdb:*
14: em_estdb:*
15: em_estdb:*
16: em_estdb:*
17: em_estdb:*
18: em_estdb:*
19: em_estdb:*
20: em_estdb:*
21: em_estdb:*
22: em_estdb:*
23: em_estdb:*
24: em_estdb:*
25: em_estdb:*
26: em_estdb:*
27: em_estdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB	ID	Description
1	231.8	98.2	413	14	W38319
2	231.8	98.2	514	9	AA131744
3	231.8	98.2	554	9	AA577318
4	231.8	98.2	703	14	BO001221
5	231.8	98.2	770	14	BO000281
6	229.8	97.4	429	14	T29172

7	228.6	96.9	375	12	B019263
8	228.6	96.9	548	14	BM957237
9	228.2	96.7	698	9	AA171571
10	227.8	96.5	424	9	AA923615
11	227.8	96.5	528	9	A1678441
12	227.2	96.3	549	9	A166941
13	227.2	96.2	521	9	A1022364
14	226.8	96.1	314	9	AA382165
15	226.2	95.8	618	10	AA273081
16	225.2	95.4	415	9	AA362146
17	223.6	94.7	817	9	A1609005
18	217.8	92.3	430	14	AA7101
19	217.8	92.3	793	14	BM999417
20	216.2	91.6	911	12	HC194765
21	209.6	88.8	223	9	AA362379
22	195	82.6	454	14	D20737
23	193.4	81.9	196	9	AA362067
24	186.2	75.9	749	12	BG117168
25	179	75.8	286	10	BE183186
26	164.4	69.7	252	10	AA779422
27	156.6	66.4	241	14	C06317
28	149.4	63.3	746	13	B1519707
29	146.2	61.9	925	10	BE19601
30	131.8	55.8	619	10	AA953756
31	118	50.0	325	14	BM734809
32	118	50.0	325	14	BM734867
33	118	50.0	335	14	BM734704
34	118	50.0	589	14	BM735183
35	118	50.0	638	14	BM734947
36	117	49.6	413	14	BM734965
37	114.4	48.5	565	13	B1961894
38	114.4	48.5	578	13	B1961760
39	114.4	48.5	689	13	B1961585
40	110.6	46.9	691	13	B1961729
41	101.4	43.0	342	14	BO600541
42	101.4	43.0	508	14	BO600473
43	99.8	42.3	343	14	BO600632
44	99.8	42.3	372	14	BO600032
45	99.8	42.3	374	14	BO600059

ALIGNMENTS

RESULT 1
W38319/C
LOCUS
DEFINITION
W38319 413 bp mRNA linear EST 15-MAY-1996
ZC77B02.s1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:328299 3'

similar to gb:M15310 INTRILINKIN-1 beta precursor (HUMAN);, mRNA
sequence.

ACCESSION
W38319
VERSION
W38319.1 GI:1319934

KEYWORDS
EST.

SOURCE
human.

ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 413)

AUTHORS
Hiller L., Lennon G., Becker M., Bonaldo M.F., Chaplin J.R.,

Chisoc S., Dietrich N., Dunogue T., Favell A., Gish W., Harkins

M., Mullum M., Kucada T., Lacy M., Le M., Le N., Maizels E., Moore

B., Morris M., Parsons J., Prange G., Rikkin L., Rohlfing T.,

Schellberg K., Soares M.B., Tan F., Thierly-Mag J., Trevisan E.,

Underwood K., Woldmann P., Waterston R., Wilson R. and Merritt M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

TITLE
JOURNAL
MEDLINE
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

FEATURES

Location/Qualifiers
1..554

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_009"
/clone="IMAGE:1075582"
/issue_type="Colon tumor KKK"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from KKK+ colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (Soares4).

BASE COUNT 176 a 97 c 126 g 154 t 1 others
ORIGIN

Query Match 98.2%; Score 231.8; DB 9; Length 554;
Best Local Similarity 99.1%; Pred. No. 1.5e-48;
Matches 233; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 TTGATTCATTCGCTCAATTAATTCAGAGGCGGCAAGACAGACAGTGTCTGTAAGAAG 61
111
DB 235 TTTTATTCATTCGCTCAATTAATTCAGAGGCGGCAAGACAGTGTCTGTAAGAAG 176
111
QY 62 CCTAGTTTAAATAGCTATGGAATCAATTCGATTTGGATGCTGCTCTCTTTAAATCA 121
111
DB 175 CCTAGTTTAAATAGCTATGGAATCAATTCGATTTGGATGCTGCTCTCTTTAAATCA 116
111
QY 122 AGTCCTTTAAATAGCTATGGAATCAATTCGATTTGGATGCTGCTCTCTTTAAATCA 181
111
DB 115 AGTCCTTTAAATAGCTATGGAATCAATTCGATTTGGATGCTGCTCTCTTTAAATCA 56
111
QY 182 AATGACCAATATGATACCTCTTCATGCTTGAATTAACCTTCAGTGAAGAAA 236
111
DB 55 AATGACCAATATGATACCTCTTCATGCTTGAATTAACCTTCAGTGAAGAAA 1

RESULT 4
LOCUS B0001221/c 793 bp mRNA linear EST 17-JUN-2002
DEFINITION UT-H-DH1-avp-9-21-0-01.s1 NCI_CGAP_DH1 Homo sapiens cDNA clone
IMAGE:5892524 3', mRNA sequence.
ACCESSION B0001221
VERSION B0001221.1 GI:19726121
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 703)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/INM at: <http://image.jim.gov>
The following repetitive elements were found in this cDNA
sequence: 221-272. >(TAAA)nSimple_repeat
Seq primer: M13 FORWARD
PolyA=yes.

FEATURES
1..703 Location/Qualifiers
/organism="Homo sapiens"

/db_xref="taxon:9606"
/clone="IMAGE:5892524"
/clone_lib="NCI_CGAP_DH1"
/issue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_DH1 is a normalized cDNA library containing the following tissues(s): V5-8 Cell line from Metastatic Chondrosarcoma in lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AATCATCTGCT.
TAG_LIB-UT-H-DH1
TAG_TISSUE-lung
TAG_SEQ-AATCATCTGCT

BASE COUNT 203 a 139 c 158 g 202 t 1 others
ORIGIN

Query Match 98.2%; Score 231.8; DB 14; Length 703;
Best Local Similarity 99.1%; Pred. No. 1.5e-48;
Matches 233; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 TTGATTCATTCGCTCAATTAATTCAGAGGCGGCAAGACAGTGTCTGTAAGAAG 61
111
DB 246 TTTTATTCATTCGCTCAATTAATTCAGAGGCGGCAAGACAGTGTCTGTAAGAAG 187
111
QY 62 CCTAGTTTAAATAGCTATGGAATCAATTCGATTTGGATGCTGCTCTCTTTAAATCA 121
111
DB 186 CCTAGTTTAAATAGCTATGGAATCAATTCGATTTGGATGCTGCTCTCTTTAAATCA 127
111
QY 122 AGTCCTTTAAATAGCTATGGAATCAATTCGATTTGGATGCTGCTCTCTTTAAATCA 181
111
DB 126 AGTCCTTTAAATAGCTATGGAATCAATTCGATTTGGATGCTGCTCTTTAAATCA 67
111
QY 182 AATGACCAATATGATACCTCTTCATGCTTGAATTAACCTTCAGTGAAGAAA 236
111
DB 66 AATGACCAATATGATACCTCTTCATGCTTGAATTAACCTTCAGTGAAGAAA 12

RESULT 5
LOCUS B0000281/c 770 bp mRNA linear EST 17-JUN-2002
DEFINITION UT-H-DPO-avt-c-13-0-01.s1 NCI_CGAP_Fs1 Homo sapiens cDNA clone
IMAGE:5884972 3', mRNA sequence.
ACCESSION B0000281
VERSION B0000281.1 GI:19725181
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 770)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mary Hendrix
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/INM at: <http://image.jim.gov>
The following repetitive elements were found in this cDNA

Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINT)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINT at:
<http://image.llnl.gov>
 Plate: LLM10219 row: a column: 10
 High quality sequence stop: 367.
 Location/Qualifiers
 1..375
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4444065"
 /clone_lib="NIH_MGC_90"
 /tissue_type="adenocarcinoma, cell line"
 /note="organ: liver; Vector: pCMV-SORT6; Site_1: Not1;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.7 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

BASE COUNT 131 a 64 c 59 g 121 t
 ORIGIN

Query Match 96.9%; Score 228.6; DB 12; Length 375;
 Best Local Similarity 98.3%; Pred. No. 9,1e-48;
 Matches 231; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TTGATTCATTCGTCGCTAATTATTCAGAGGGGCGCAGACAGTCGCTGTAAGAAG 61
 Db 119 TTTATTCATTCGTCGCTAATTATTCAGAGGGGCGCAGACAGTCGCTGTAAGAAG 178
 QY 62 CCTAGTTTAAAGCTATGAGATCAATTCATTTGCGCTGCTGCTCTTTAATCA 121
 Db 179 CCTAGTTTAAAGCTATGAGATCAATTCATTTGCGCTGCTGCTCTTTAATCA 238
 QY 122 AGTCCTTTAATAGACTGAAATATATAGCTGACATTTTAAATGGAATATTATA 181
 Db 239 AGTCCTTTAATAGACTGAAATATATAGCTGACATTTTAAATGGAATATTATA 298
 QY 182 AATGACCAATATGATACGTCGATGCTGCAATTAACCTGACAGGAGAAA 236
 Db 299 AATGACCAATATGATACGTCGATGCTGCAATTAACCTGACAGGAGAAA 353

RESULT 8
 BM997237 548 bp mRNA linear EST 17-JUN-2002
 LOCUS U1-H-DHO-aug-03-0-01.s1 NC1-CCAP-DHO Homo sapiens cDNA clone
 DEFINITION IMAGE:5872130 3', mRNA sequence.
 ACCESSION BM997237
 VERSION BM997237.1 GI:19722138
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 548)
 N1-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)

JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jose Mercunede
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINT at: <http://image.llnl.gov>
 The following repetitive elements were found in this cDNA

sequence: 221-272, >(TAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLYA-yes.
 Location/Qualifiers
 1..548
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5872130"
 /clone_lib="NC1-CCAP-DHO"
 /tissue_type="Metastatic Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /note="organ: lung; Vector: p1773-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 NC1-CCAP-DHO is a cDNA library containing the following
 tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma
 in lung. The library was constructed according to Bonaldi,
 Lennon and Soares, Genome Research, 6:791-806, 1996. First
 strand cDNA synthesis was primed with an oligo-dT primer
 containing a Not I site. Double stranded cDNA was ligated
 to an EcoR I adaptor, digested with Not I, and cloned
 directionally into p1773-Pac vector. The oligonucleotide
 used to prime the synthesis of first-strand cDNA contains
 a library tag sequence that is located between the Not I
 site and the (dT)18 tail. The sequence tag for this
 library is ACATCATTCG.
 TAG_L1B-U1-H-DHO
 TAG_P1SSUE-lung
 TAG_SEQ-ACATCATTCG"

BASE COUNT 172 a 95 c 123 g 158 t
 ORIGIN

Query Match 96.9%; Score 228.6; DB 14; Length 548;
 Best Local Similarity 98.3%; Pred. No. 9,4e-48;
 Matches 231; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TTGATTCATTCGTCGCTAATTATTCAGAGGGGCGCAGACAGTCGCTGTAAGAAG 61
 Db 246 TTTATTCATTCGTCGCTAATTATTCAGAGGGGCGCAGACAGTCGCTGTAAGAAG 187
 QY 62 CCTAGTTTAAAGCTATGAGATCAATTCATTTGCGCTGCTGCTCTTTAATCA 121
 Db 186 CCTAGTTTAAAGCTATGAGATCAATTCATTTGCGCTGCTGCTCTTTAATCA 127
 QY 122 AGTCCTTTAATAGACTGAAATATATAGCTGACATTTTAAATGGAATATTATA 181
 Db 126 AGTCCTTTAATAGACTGAAATATATAGCTGACATTTTAAATGGAATATTATA 67
 QY 182 AATGACCAATATGATACGTCGATGCTGCAATTAACCTGACAGGAGAAA 236
 Db 66 AATGACCAATATGATACGTCGATGCTGCAATTAACCTGACAGGAGAAA 12

RESULT 9
 A1471571 698 bp mRNA linear EST 14-APR-1999
 LOCUS U198h09.x1 NC1-CCAP-C014 Homo sapiens cDNA clone IMAGE:2155169 4'
 DEFINITION similar to gb:M15140 INTERLUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
 sequence.
 ACCESSION A1471571
 VERSION A1471571.1 GI:4333661
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 698)
 NC1-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)

JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

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OM nucleic : nucleic search, using sw model

Run on: March 17, 2003, 20:34:55 ; Search time 1462 Seconds
(without alignments)
2614.319 Million cell updates/sec

Title: US-09-247-874c-2_COPY_8710_8945

Perfect score: 236
Sequence: 1 tttagatcatgctcctat.....ataacttcacttaaaaaa 236

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estma:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: qb_est1:*
10: qb_est2:*
11: qb_hic:*
12: qb_est3:*
13: qb_est4:*
14: qb_est5:*
15: em_estfun:*
16: em_estom:*
17: qb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	189	80.1	324	AA923615 ng98b03.s
2	189	80.1	413	W38319 W38319
3	189	80.1	514	AA131744 AA131744
4	189	80.1	521	AI022364 AI022364
5	189	80.1	528	AI678441 AI678441
6	189	80.1	548	BM997237 BM997237

C 7	189	80.1	554	9	AA57318	AA57318 um99408.s
C 8	189	80.1	618	10	AM273081	AM273081 x027h01.x
C 9	189	80.1	703	14	H0001221	H0001221 U1-H-DH1-
C 10	189	80.1	770	14	H0000281	H0000281 U1-H-DH1-
C 11	189	80.1	817	9	A1609005	A1609005 tW85407.x
C 12	189	80.1	911	12	BC194765	BC194765 RST34064
C 13	147	62.3	549	9	A1566931	A1566931 t97b02.x
C 14	147	62.3	746	13	B1519707	B1519707 603061928
C 15	143	60.6	793	14	BM999417	BM999417 U1-H-DH0-
C 16	138	58.5	314	9	AA382165	AA382165 H5195428
C 17	138	58.5	375	12	BC119263	BC119263 602346146
C 18	138	58.5	698	9	A1471571	A1471571 t198b09.x
C 19	136	57.6	429	14	T29172	T29172 EST71208.Hu
C 20	130	55.1	415	9	AA362146	AA362146 EST18110
C 21	130	55.1	749	12	BC117168	BC117168 602346146
C 22	125	53.0	454	14	D20737	D20737 HUMS01714
C 23	124	52.5	223	9	AA362379	AA362379 EST181846
C 24	113	47.9	619	10	AW953756	AW953756 EST365826
C 25	108	45.8	430	14	W47101	W47101 ZC39B04.s1
C 26	107	45.3	196	9	AA362067	AA362067 EST71531
C 27	97	41.1	241	14	C06317	C06317 C06317.Homa
C 28	93	39.4	284	10	BE183186	BE183186 RC4-H1066
C 29	61	25.8	925	10	BE619601	BE619601 603472703
C 30	51	21.6	252	10	AW779422	AW779422 h094409.x
C 31	31	13.1	259	12	BS058513	BS058513 h0115002
C 32	28	11.9	265	10	BE181337	BE181337 RC4-H1066
C 33	24	10.2	703	10	AV715551	AV715551 AV715551
C 34	23	9.7	360	9	AA916006	AA916006 c086407.s
C 35	22	9.3	559	17	BS958295	BS958295 B087P47TR
C 36	20	8.5	685	17	AC163910	AC163910 Pan t0041
C 37	20	8.5	993	17	CNS060CR	AL407905.T7 end of
C 38	19	8.1	300	14	C53301	C53301 C53301.YuJ1
C 39	19	8.1	381	17	A236878	A236878 RPT-21-9
C 40	19	8.1	463	13	H0148984	H0148984 B0148984
C 41	19	8.1	476	14	BM864065	BM864065 m9cm08XB
C 42	19	8.1	583	17	BM674814	BM674814 B0MEG17TR
C 43	19	8.1	616	17	A0436473	A0436473 HS-5052.B
C 44	19	8.1	646	12	BS809864	BS809864 m04c001xm
C 45	19	8.1	661	10	AV702246	AV702246 AV702246

ALIGNMENTS

RESULT 1
AA923615/c
LOCUS
DEFINITION
ng98b03.s1 NCI-CCAP_Colo Homo Sapiens cDNA clone IMACB:1160333.3'
similar to gb:U15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA

ACCESSION
AA923615
VERSION
AA923615.1 GI:3070924
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 324)
AUTHORS
Mamallay; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Euteleostomi; Primates; Catarrhini; Homidae; Homo.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-i@mail.nih.gov
Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck, M.D.
Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILIN. at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 1123 Std Error: 0.00

Seq primer: 40m13 fwd. EF from AmerSham
High quality sequence stop: 214.
Location/Qualifiers
1..324

FEATURES
Source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1160343"
/clone_lib="NCI-GAP_Col0"
/issue_type="colon tumor RER"
/lab_host="HEp03"
/note="Organ: colon; Vector: pF73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pF73 vector. Library is normalized. Library was constructed by Brent Soares and M. Fatima Bonaldo (N Soares)."
BASE COUNT 117 a 55 c 57 g 95 t
ORIGIN

Query Match 80.1%; Score 189; Dn 9; Length 324;
Best Local Similarity 100.0%; Pred. No. 76-94;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 ATTGATGGCTGATTTATGTAAGGGGCTAGAGAGTGCCTGCTAAAGAGGCTA 65
|||||
227 ATGATGGCTGATTTATGTAAGGGGCTAGAGAGTGCCTGCTAAAGAGGCTA 168
|||||
66 GTTTTAAAGCTATGGAATCAATTCATTGACGCTGCTGCTCTTAAATCAAGTC 125
|||||
167 GTTTTAAAGCTATGGAATCAATTCATTGACGCTGCTGCTCTTAAATCAAGTC 108
|||||
66 GTTTTAAAGCTATGGAATCAATTCATTGACGCTGCTGCTCTTAAATCAAGTC 125
|||||
126 GTTTTAAAGCTATGGAATCAATTCATTGACGCTGCTGCTCTTAAATCAAGTC 185
|||||
107 GTTTTAAAGCTATGGAATCAATTCATTGACGCTGCTGCTCTTAAATCAAGTC 48
|||||
186 AGCAAAATAT 194
|||||
47 AGCAAAATAT 49

RESULT 2
W48419/c 413 bp mRNA linear EST 15-MAY-1996
L48305
DEFINITION
207702.s1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:328299 3'
similar to gb:U15340 INTERLEUKIN-1 BETA PRECURSOR (HUMAN); mRNA
sequence.
W48419
ACCESSION
W48419.1 GI:119944
VERSION
W48419.1 GI:119944
KEYWORDS
EST
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 413)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chipelli, B.,
Christie, S., Dietrich, N., Dubugue, T., Favello, A., Gish, W., Hawkins,
M., Hulman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Martin, E., Moore,
J., Morris, M., Parsons, J., Prange, C., Rikkin, L., Rohlfing, T.,
Schellhammer, K., Soares, M.B., Tan, F., Thierrey-Mieg, J., Trevisan, E.,
Underwood, K., Weidmann, P., Waterston, R., Wilson, R. and Murtu, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9): 807-828 (1996)
9704478
Contact: Wilson R
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est-watson.wustl.edu
This clone is available royalty-free through LIND; contact the
IMAGE Consortium (info@image.lind.gov) for further information.

Seq primer: mb1.REV44ET
High quality sequence stop: 368.
Location/Qualifiers
1..413

FEATURES
Source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="IMAGE:1262704"
/clone="IMAGE:428299"
/clone_lib="pancreatic islet"
/issue_type="pancreatic islet"
/lab_host="BHK cells (kanamycin resistant)"
/note="Organ: pancreas; Vector: phage vector SK+ (Site 1);
EcoRI Site 2; Abot; Reference: Hum Mol Gen 2, 1795 (1993)
Takeda et al. Cloned and functionally primed; oligo dT
5' adaptor sequence: 5' GAAATGGGAGAG 3' 3' adaptor
sequence: 5' GCAATGTTTCTTTTCTTTT 3'
BASE COUNT 135 a 65 c 86 g 127 t
ORIGIN

Query Match 80.1%; Score 189; Dn 14; Length 413;
Best Local Similarity 100.0%; Pred. No. 7-20-94;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 ATTGATGGCTGATTTATGTAAGGGGCTAGAGAGTGCCTGCTAAAGAGGCTA 65
|||||
239 ATGATGGCTGATTTATGTAAGGGGCTAGAGAGTGCCTGCTAAAGAGGCTA 180
|||||
66 GTTTTAAAGCTATGGAATCAATTCATTGACGCTGCTGCTCTTAAATCAAGTC 125
|||||
179 GTTTTAAAGCTATGGAATCAATTCATTGACGCTGCTGCTCTTAAATCAAGTC 120
|||||
126 GTTTTAAAGCTATGGAATCAATTCATTGACGCTGCTGCTCTTAAATCAAGTC 185
|||||
119 GTTTTAAAGCTATGGAATCAATTCATTGACGCTGCTGCTCTTAAATCAAGTC 60
|||||
186 AGCAAAATAT 194
|||||
59 AGCAAAATAT 51

RESULT 3
AA131744/c 514 bp mRNA linear EST 27-NOV-1996
L48305
DEFINITION
2135102.s1 Soares-pregnant uterus NHEK Homo sapiens cDNA clone
IMAGE:503931 3' similar to gb:U15340 INTERLEUKIN-1 BETA PRECURSOR
(HUMAN); mRNA sequence.
AA131744
ACCESSION
AA131744.1 GI:1693270
VERSION
AA131744.1 GI:1693270
KEYWORDS
EST
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 514)
Hillier, L., Clark, N., Dubugue, T., Ellington, K., Hawkins, M., Hulman,
M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Murtu, M., Parsons, J.,
Rikkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston,
R., Williamson, A., Weidmann, P., and Wilson, R.
The WashU-Marc EST Project
Unpublished (1995)
Contact: Wilson R
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est-watson.wustl.edu
This clone is available royalty-free through LIND; contact the
IMAGE Consortium (info@image.lind.gov) for further information.
Seq primer: 40m13 fwd. from AmerSham
High quality sequence stop: 277.
Location/Qualifiers
1..514
/organism="Homo sapiens"

```

/db_xref="GDB:3808919"
/db_xref="taxon:9606"
/clone_image="503931"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: uterus; Vector: p773-Pac; Site: 1; Not 1;
Site 2: Eco RI; 1st strand cDNA was primed with a Not 1 -
oligo(dT) primer [5',
AACTGAGAGATTCGGCGCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(pharmacia), digested with Not 1 and cloned into the Not 1
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."
BASE COUNT      156 a      85 c      114 g      149 t      10 others
ORIGIN
Query Match      80.1%; Score 189; DB 9; Length 514;
Best Local Similarity 100.0%; Pred. No. 7.4e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6  ATTCATTGCTCTAATTATTCGAAGCGCGCAGAGTAGCAGTCTGTAAAGACCTTA 65
        |||||||
DB      244 ATTCATTGCTCTAATTATTCGAAGCGCGCAGAGTAGCAGTCTGTAAAGACCTTA 185

QY      66  GTTTTAAATAGCTATGGAATCAATTCATTGGACGTGCTGCTCTTTAAATCAAGTC 125
        |||||||
DB      184 GTTTTAAATAGCTATGGAATCAATTCATTGGACGTGCTGCTCTTTAAATCAAGTC 125

QY      126 CTTTAATTAAGCTGAAATATATATAGCTCAGATTATTAAATGGCAATTTATAATG 185
        |||||||
DB      124 CTTTAATTAAGCTGAAATATATATAGCTCAGATTATTAAATGGCAATTTATAATG 65

QY      186 AGCAATAT 194
        |||||||
DB      64 AGCAATAT 56

RESULT 4
LOCUS      A1022364      521 bp      mRNA      linear      EST 28-AUG-1998
DEFINITION o664405.x1 Soares_senescen-fibroblasts_NBHSF Homo sapiens cDNA
            clone IMAGE:1651640 3' similar to gb:M15330 INTERLEUKIN-1 BETA
            PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION  A1022364
VERSION     A1022364.1  GI:3237605
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 521)
            NC-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cyabbs@mail.nih.gov
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1077 Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amer sham
            High quality sequence stop: 403.
FEATURES
            source
            1..521
            location/Qualifiers
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_image="1651640"
            /clone_lib="Soares_senescen-fibroblasts_NBHSF"
            /tissue_type="senescent fibroblast"
            /lab_host="DH10B (ampicillin resistant)"

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/notes="Vector: p773) (pharmacia) with a modified
polylinker V-type; phagmid; Site: 1; Not 1; Site 2: Eco RI
polylinker V-type; phagmid; Site: 1; Not 1; Site 2: Eco RI
primer [5',
TGTACCAATCTGAACTGGAGCGCGCATTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (pharmacia), digested with Not 1 and cloned into
the Not 1 and Eco RI sites of a modified p773 vector
(pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Renato
Soares and M. Fatima Bonaldo."
BASE COUNT      165 a      92 c      123 g      141 t
ORIGIN
Query Match      80.1%; Score 189; DB 9; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.4e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6  ATTCATTGCTCTAATTATTCGAAGCGCGCAGAGTAGCAGTCTGTAAAGACCTTA 65
        |||||||
DB      232 ATTCATTGCTCTAATTATTCGAAGCGCGCAGAGTAGCAGTCTGTAAAGACCTTA 173

QY      66  GTTTTAAATAGCTATGGAATCAATTCATTGGACGTGCTGCTCTTTAAATCAAGTC 125
        |||||||
DB      172 GTTTTAAATAGCTATGGAATCAATTCATTGGACGTGCTGCTCTTTAAATCAAGTC 113

QY      126 CTTTAATTAAGCTGAAATATATATAGCTCAGATTATTAAATGGCAATTTATAATG 185
        |||||||
DB      112 CTTTAATTAAGCTGAAATATATATAGCTCAGATTATTAAATGGCAATTTATAATG 53

QY      186 AGCAATAT 194
        |||||||
DB      52 AGCAATAT 44

RESULT 5
LOCUS      A1678441      528 bp      mRNA      linear      EST 15-DEC-1994
DEFINITION tu82d01.x1 NC-CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257537 3'
            similar to gb:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
            sequence.
ACCESSION  A1678441
VERSION     A1678441.1  GI:4888623
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 528)
            NC-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cyabbs@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael K.
            Emmert-Buck, M.D., Ph.D.
            CDNA Library Preparation: Life Technologies, Inc.
            DNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NC-CGAP clone distribution information can be
            found through the T.M.A.C.R. Consortium/LLNL at:
            www-bio.llnl.gov/btrp/image/image.html
            Insert length: 1763 Std Error: 0.00
            Seq primer: -40up from Gibco
            High quality sequence stop: 404.
FEATURES
            source
            1..528
            location/Qualifiers
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_image="2257537"
            /clone_lib="NC-CGAP_Gas4"
            /tissue_type="poorly differentiated adenocarcinoma with

```

signal ring cell features"
 /lab host="DH108"
 /note="Organ: stomach; Vector: pCMV-Sport6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. primer: Oligo dt.
 Average insert size 1.69 kb. Ligo Technologies catalog #: 11549-011"
 BASE COUNT 172 a 98 c 117 g 140 t 1 others
 ORIGIN
 Query Match 80.1%; Score 189; DB 9; Length 528;
 Host Local Similarity 100.0%; Prod. No. 7,40-93;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 ATTGATGGTCTAATTATTCAGAGGGGCAAGAGTACAGCTCTGTAAGACAGCTTA 65
 11549-011 11549-011 11549-011 11549-011 11549-011 11549-011
 Db 227 ATTGATGGTCTAATTATTCAGAGGGGCAAGAGTACAGCTCTGTAAGACAGCTTA 168
 QY 66 GTTTTAAATAGCTATGATCAATTCATTCAGCTGCTGCTCTTTAAATCAAGTC 125
 11549-011 11549-011 11549-011 11549-011 11549-011 11549-011
 Db 167 GTTTTAAATAGCTATGATCAATTCATTCAGCTGCTGCTCTTTAAATCAAGTC 108
 QY 126 GTTTTAAATAGCTATGATCAATTCATTCAGCTGCTGCTCTTTAAATCAAGTC 185
 11549-011 11549-011 11549-011 11549-011 11549-011 11549-011
 Db 107 GTTTTAAATAGCTATGATCAATTCATTCAGCTGCTGCTCTTTAAATCAAGTC 48
 QY 186 AGCAAAATAT 194
 11549-011 11549-011 11549-011 11549-011 11549-011 11549-011
 Db 47 AGCAAAATAT 39
 11549-011 11549-011 11549-011 11549-011 11549-011 11549-011
 RESULT 6 548 bp mRNA linear EST 17-JUN-2002
 BM997237
 LOCUS U1-H-DHO-auc-f-03-0-01.st.NC1_CGAP_DHO Homo sapiens cDNA clone
 DEFINITION IMAGE:5872130.3', mRNA sequence.
 ACCESSION BM997237 GI:19722138
 VERSION BM997237.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 548)
 AUTHOR NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs@mail.nih.gov
 Tissue procurement: Dr. Jose Meric-Bend
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA sequencing by: Dr. M. Bento Soares, University of Iowa
 clone distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/HLIN at: http://image.hlin.gov
 The following repetitive elements were found in this cDNA
 sequence: 221-272: (TTAA)n (simple-repeat)
 Seq primer: M13 FORWARD
 Polya Yes.
 FEATURES
 SOURCE location/Qualifiers
 1..548
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5872130"
 /clone_1ib="NC1_CGAP_DHO"
 /issue_type="Metastatic Chondrosarcoma"
 /lab_host="DH108" (Life Technologies)
 /note="Organ: lung; Vector: pTZ19-Pac (Pharmacia) with a
 modified polylinker; Site_1: PstI; Site_2: NotI;
 NC1_CGAP_DHO is a cDNA library containing the following
 tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma
 in lung. The library was constructed according to Bonaldo,

Lennon and Soares, Genome Research, 6:791-806, 1996. PstI
 strand cDNA synthesis was primed with an oligo dt primer
 containing a NotI site. Double stranded cDNA was ligated
 to an EcoRI adaptor, digested with NotI, and cloned
 directionally into pTZ19-Pac vector. The oligonucleotide
 used to prime the synthesis of first strand cDNA contains
 a library tag sequence that is located between the NotI
 site and the (GT)18 tail. The sequence tag for this
 library is AGATCATGGC.
 TAG_1lib-01-H-DHO
 TAG_1ISSUE lung
 TAG_SEQ AGATCATGGC"
 BASE COUNT 172 a 95 c 123 g 158 t
 ORIGIN
 Query Match 80.1%; Score 189; DB 14; Length 548;
 Host Local Similarity 100.0%; Prod. No. 7,50-93;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 ATTGATGGTCTAATTATTCAGAGGGGCAAGAGTACAGCTCTGTAAGACAGCTTA 65
 11549-011 11549-011 11549-011 11549-011 11549-011 11549-011
 Db 242 ATTGATGGTCTAATTATTCAGAGGGGCAAGAGTACAGCTCTGTAAGACAGCTTA 183
 QY 66 GTTTTAAATAGCTATGATCAATTCATTCAGCTGCTGCTCTTTAAATCAAGTC 125
 11549-011 11549-011 11549-011 11549-011 11549-011 11549-011
 Db 182 GTTTTAAATAGCTATGATCAATTCATTCAGCTGCTGCTCTTTAAATCAAGTC 123
 QY 126 GTTTTAAATAGCTATGATCAATTCATTCAGCTGCTGCTCTTTAAATCAAGTC 185
 11549-011 11549-011 11549-011 11549-011 11549-011 11549-011
 Db 122 GTTTTAAATAGCTATGATCAATTCATTCAGCTGCTGCTCTTTAAATCAAGTC 63
 QY 186 AGCAAAATAT 194
 11549-011 11549-011 11549-011 11549-011 11549-011 11549-011
 Db 62 AGCAAAATAT 54
 11549-011 11549-011 11549-011 11549-011 11549-011 11549-011
 RESULT 7 554 bp mRNA linear EST 12-SEP-1997
 AA577318/c
 LOCUS nm83a08.st NC1_CGAP CGO Homo sapiens cDNA clone IMAGE:1075482.3'
 DEFINITION similar to gb:M15330 INTEREDIN-1 BETA PRECURSOR (HUMAN);, mRNA
 sequence.
 ACCESSION AA577318 GI:2454792
 VERSION AA577318.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 554)
 AUTHOR NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs@mail.nih.gov
 Tissue procurement: Ian Kirsch, M.D., Michael R. Emmert Buck, M.D.,
 et al.
 cDNA library preparation: M. Bento Soares, Ph.D.
 cDNA library arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome
 clone distribution: NC1_CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/HLIN at:
 www.bio.hlin.gov/brp/image/image.html
 Insert length: 1551 Std Error: 0.00
 Seq primer: 40m31 fwd. ET from Amersham
 High quality sequence stop: 414.
 FEATURES
 SOURCE location/Qualifiers
 1..554
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1075482"
 /clone_1ib="NC1_CGAP_CGO"

/tissue_type="colon tumor REK-"
/lab_host="DBH108"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from REK- colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (Soares4)."

BASE COUNT 176 a 97 c 126 g 154 t 1 others
ORIGIN

Query Match 80.1%; Score 189; DB 9; Length 554;
Best Local Similarity 100.0%; Pred. No. 7.5e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATGCTTAATTTATTCGAAGGGGGGAGAGTGCAGTAAAGAGCCGA 65
|||||
DB 241 ATTCATGCTTAATTTATTCGAAGGGGGGAGAGTGCAGTAAAGAGCCGA 172
QY 66 GTTTTAATGCTATGATCAATTCATTCAGTGTGCTCTTTAATCAAGTC 125
|||||
DB 171 GTTTTAATGCTATGATCAATTCAGTGTGCTCTTTAATCAAGTC 112
QY 126 GTTTTAATGCTATGATCAATTCAGTGTGCTCTTTAATCAAGTC 185
|||||
DB 111 GTTTTAATGCTATGATCAATTCAGTGTGCTCTTTAATCAAGTC 52
QY 186 ACCAATAT 194
|||||
DB 51 ACCAATAT 43

RESULT 8
AM273081/c
LOCUS x027h01.x1 NC1-CCAP_Co14 Homo sapiens cDNA clone IMAGE:2801425 3'
DEFINITION similar to gp:M15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA
ACCESSION AM273081
VERSION AM273081.1 GI:6660111
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 618)
TITLE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Bunker-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILIN. at:
www.bio.lnlnl.gov/btrp/image/image.html

FEATURES
Source
1..618
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2801425"
/clone_lib="NCI-CCAP_Co14"

Possible reversed clone: polYT not found
Seq primer: -400P from Gibco
High quality sequence stop: 399.

/tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DBH108"
/note="Organ: colon; Vector: pCMV-SpRpbT; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.7 kb. Life Technologies catalog #: 11531-019"

BASE COUNT 193 a 121 c 137 g 167 t
ORIGIN

Query Match 80.1%; Score 189; DB 10; Length 618;
Best Local Similarity 100.0%; Pred. No. 7.6e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATTCATGCTCTAATTTATTCGAAGGGGGGAGAGTGCAGTAAAGAGCCGA 65
|||||
DB 227 ATTCATGCTCTAATTTATTCGAAGGGGGGAGAGTGCAGTAAAGAGCCGA 168
QY 66 GTTTTAATGCTATGATCAATTCATTCAGTGTGCTCTTTAATCAAGTC 125
|||||
DB 167 GTTTTAATGCTATGATCAATTCATTCAGTGTGCTCTTTAATCAAGTC 108
QY 126 GTTTTAATGCTATGATCAATTCATTCAGTGTGCTCTTTAATCAAGTC 185
|||||
DB 107 GTTTTAATGCTATGATCAATTCATTCAGTGTGCTCTTTAATCAAGTC 48
QY 186 ACCAATAT 194
|||||
DB 47 ACCAATAT 39

RESULT 9
B0001221/c
LOCUS U1-H-DH1-awp-g-21-0-01.s1 NCI-CCAP-DH1 Homo sapiens cDNA clone
DEFINITION IMAGE:5892524 3', mRNA sequence.
ACCESSION B0001221
VERSION B0001221.1 GI:19726121
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 703)
TITLE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/ILIN. at: http://image.lnlnl.gov
The following repetitive elements were found in this cDNA sequence: 221-272, >(TAA)n*Simple.Repeat
Seq primer: M13 FORWARD
POLY-A=yes.

FEATURES
Source
1..703
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5892524"
/clone_lib="NCI-CCAP-DH1"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DBH108 (Life Technologies)"
/note="Organ: Lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI-CCAP-DH1 is a normalized cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed

HASH: COINTEGRATION	2013	139	158	202	1 others
ORIGIN					

Query Match 80.1%; Score 189; DB 14; Length 703;
 Best Local Similarity 100.0%; Prod. No. 7.7e-93;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 ATTCTATTCTCTCTAATTTATTCTAAAGCGGGCAGAGACTAGCAGCTGTCTGTCTGTTAAAGAGCGCTA 65

[illegible]

182 GTTTTAAACCTATGGAATCAATTCATTTCGACCTGGTGTCTTCCTTAAATCAACTTC 12

126 CTTTAATTAGAGCTGAAAATATATTAAGCTCAGACTTATTTAAATCGGATAATTATTAATG 18

1964

[illegible]

RESULT 10

Accession	Length	Source	Accession	Length	Source
U00002.1	770 bp	mtDNA	U00002.1	770 bp	mtDNA

ATTENTION: IMAGE:58849/2-3', mirna sequence, HQ000281

KEYWORDS:
Selling
human
body

Phylum: Chordata; Class: Craniata; Order: Vertebrata; Suborder: Euteleostomi; Superorder: Osteichthyes; Class: Actinopterygii; Order: Cyprinodontiformes; Family: Poeciliidae; Genus: *Gambusia*; Species: *Gambusia holbrooki*.

REFERENCE 1 (bases 1 to 770)
 AUTHORS N1 (CASP <http://www.ncbi.nlm.nih.gov/ncicgap>,

Tumor Gene Index
[Prothlisboed (1997)]
[offprint]

Email: cquappes-76@mail.nih.gov

cDNA library preparation: Dr. M. Bento Soares, University of
cDNA library Arrayed by: Dr. M. Bento Soares, University of

Clone distribution: clone distribution information can be obtained through the MAQ file (consortium/MAQfile.htm) [10].

The following repetitive elements were found in this cDNA sequence: 221-272, \times (TAA)n#simple_repeat.

FEATURES
POLYA YOS,
Location/Qualifiers

4th grad "Homo sapiens"
/organism "Homo sapiens"

```

/clohe-2 IMAGE:58839/2"
/clohe-11b- "NCL CGAP_PSL"

```

/ lab_host - "MILIB (Life Technologies)"

/note Vector: pT73-Pac (Pharmacia) with a modified polymerase; Site_1: EcoR I; Site_2: Not I; Not_CAT_Fast is a cDNA library containing the following tissues(s): Fibrosarcoma Cell Line HT-1080 (ATCC number CCL 121). The library was constructed according to Bonaldi, Jenson and Sources, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo d(T)₁₈ primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The 1st round pool was used to prime the synthesis of first-strand cDNA containing a library tail sequence that is located between the Not I site and the (d(T))₁₈ tail). The sequence TGGTCTGTTTC

```

TAG_LIB-01-H-1P1)
TAG_TISSUE libosd.com
TAG_LIB-01-H-1P1)

```

HASTE COUNT	ORIGIN
218 d	148 c
177 a	224 f
300 b	300 h

Query Match	80.1%; Score 189; DB 14; Length 770;
Best Local Similarity	100.0%; Pred. No. 7.8e 93;

[illegible]

Db 242 ATTATTCGCTCAATTTATTCAACGGGCGCAGAGATATCAGTGTCTTTAAACAGCTTA 183

66 GTTTTAAATAGCTATGCAATCAATTCGAATTCATCTCTCTTAAATTAAGTCG 125

[illegible]

122 CTTATATAGACCTGAAATATATAGCTCAGATTATTAAATGGGAAATATTATATATG 63

09	186	ACCTAAATAT	194

[illegible]

RESUL 11
A1609005/c*

DEFINITION 1. tw5107.x1 NCBI_CGAP_HUGO Homo Sapiens cDNA clone IMAGE:266524 4' similar to cM15.330 (HUMAN PINK1 / PINK1-RELATED KINASE (HUMAN)). mRNA

ACCESSION **Suppl no.**
A1603005

KEYWORDS	EST.
SOURCE	human

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Artiodactyla; Cetartiodactyla; Carnivora; Canidae; Mustelidae

REFERENCE
1 (bases 1 to 817)
AUTHORS
NCI/NIDK-CCAP <http://www.ncbi.nlm.nih.gov/nciccap>.

Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 (published 1997)

Final: cygabs-r@mail.nih.gov
 Title: Development of a Chlamydia Test
 Mary May
 Silvio

Gutkind, Ph.D., Myung Hoe Park, PhD,
cDNA Library Preparation, Stratagene, Inc.

DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution; MT-CGAP clone distribution information can be

www.bio.1in1.gov/bbrr/image/image.html

Seq primer: -40bp from 6160
High quality sequence stop: 441

FEATURES

Location/Qualifiers

1. 817

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="IMAGE:2265524"

/issue_type="normal glandula (cell line from primary keratinocytes)"

/lab_host="SOLR (kanamycin resistant)"

/note="Vector: Bluescript SK-; Site: 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 Kb. 5' adaptor sequence: 5' AATCGCGACG 3' GCCGCTC 5' 3' adaptor sequence: 5' (GA)10ACTAGTCTGCAGTTTCTTTT 3' EcoRI site appears to have been lost in a fraction of the clones. Library constructed by Stragene; available through Mary May, PhD (Oral and Pharyngeal Cancer Branch, National Institute of Dental and Craniofacial Research, NIH; mmay@yoda.nidcr.nih.gov)."

6 others

BASE COUNT

230 a 163 c 187 g 231 t

6 others

Query Match

80.1%; Score 189; DB 9; Length 817;

Best Local Similarity 100.0%; Pred. No. 7.9e-93;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB

6 ATTCATTGCTGTAATTATTATTCGAAGGGGCAAGAGTAGCAGTCTCTGTAAGAGCCTA 65

DB

229 ATTCATTGCTGTAATTATTATTCGAAGGGGCAAGAGTAGCAGTCTCTGTAAGAGCCTA 170

DB

66 GTTTTAATAGCTATGCAATCAATTCATTTGACGTGGTGGTCTCTTTAAATCAAGTC 125

DB

169 GTTTTAATAGCTATGCAATCAATTCATTTGACGTGGTGGTCTCTTTAAATCAAGTC 110

DB

126 GTTTTAATAGCTATGCAATCAATTCATTTGACGTGGTGGTCTCTTTAAATCAAGTC 185

DB

109 GTTTTAATAGCTATGCAATCAATTCATTTGACGTGGTGGTCTCTTTAAATCAAGTC 50

DB

186 AGCAATAT 194

DB

49 AGCAATAT 41

RESULT 12

BC194765/c 911 bp mRNA linear EST 21-APR-2001

LOCUS

BC194765 RST14064 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION

BC194765.1 GI:13716560

VERSION

EST.

KEYWORDS

human.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 911)

AUTHORS

Harrington, J.J., Sher, B., Rundle, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whitlington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Kliska, A., Hess, J., Colburn, K., Lo, K., Offenbacher, J., Danzig, J., and Ducar, M.

TITLE

Creation of genome-wide protein expression libraries using random activation of gene expression

JOURNAL

Nat. Biotechnol. 19 (5), 440-445 (2001)

MEDLINE

21227151

COMMENT

Contact: Scott J. Cain

FEATURES

3201 Carnegie Ave, Cleveland, OH 44115, USA

SOURCE

1. 911

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Athersys RAGE Library"

/cell_line="H1080"

/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances."

BASE COUNT

254 a 184 c 219 g 254 t

Query Match

80.1%; Score 189; DB 12; Length 911;

Best Local Similarity 100.0%; Pred. No. 8e-93;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB

6 ATTCATTGCTGTAATTATTATTCGAAGGGGCAAGAGTAGCAGTCTCTGTAAGAGCCTA 65

DB

229 ATTCATTGCTGTAATTATTATTCGAAGGGGCAAGAGTAGCAGTCTCTGTAAGAGCCTA 170

DB

66 GTTTTAATAGCTATGCAATCAATTCATTTGACGTGGTGGTCTCTTTAAATCAAGTC 125

DB

169 GTTTTAATAGCTATGCAATCAATTCATTTGACGTGGTGGTCTCTTTAAATCAAGTC 110

DB

126 GTTTTAATAGCTATGCAATCAATTCATTTGACGTGGTGGTCTCTTTAAATCAAGTC 185

DB

109 GTTTTAATAGCTATGCAATCAATTCATTTGACGTGGTGGTCTCTTTAAATCAAGTC 50

DB

186 AGCAATAT 194

DB

49 AGCAATAT 41

RESULT 13

AI566931/c 549 bp mRNA linear EST 13-MAY-1999

LOCUS

AI566931 LG67H02.x1 NCI-CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2213907 3'

DEFINITION

similar to gb:U15330 INTERLEUKIN-1 BETA PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION

AI566931.1 GI:4525383

VERSION

EST.

KEYWORDS

human.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 549)

AUTHORS

NCI-CGAP http://www.nci.nih.gov/ncicgap.

TITLE

Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.

FEATURES

www.bio.lnl.gov/bdip/image/image.html

SOURCE

1. 549

FEATURES

Location/Qualifiers

SOURCE

1. 549

FEATURES

/organism="Homo sapiens"

SOURCE

/db_xref="taxon:9606"

FEATURES

/clone_lib="IMAGE:2213907"

/issue_type="squamous cell carcinoma, poorly"

a library tag sequence that is located between the Not I
site and the (GT)₁₈ tail. The sequence tag for this
library is GTCTACGAG.

TAG_LIB=UT-H-DPO

TAG_TISSUE=fibrosarcoma

TAG_SEQ=GTCTACGAG

BASE COUNT 224 a 154 c 181 g 231 t 3 others
ORIGIN

Query Match 60.6%; Score 143; DB 14; length 793;

Best Local Similarity 100.0%; Pred. No. 1.5e-67;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 6 ATTGATTGGTCTAATTATTCAGAGCGGCGAGAGTAGCAGTGTCTGTAAAGAGCCTA 65
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 240 ATTGATTGGTCTAATTATTCAGAGCGGCGAGAGTAGCAGTGTCTGTAAAGAGCCTA 181
    ||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 66 GTTTTAAATAGCTATGCAATTCATTCATTTGGACTGCTGCTGCTTAAATCAAGTC 125
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 180 GTTTTAAATAGCTATGCAATTCATTCATTTGGACTGCTGCTGCTTAAATCAAGTC 121
    ||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 126 CTTTAAATAGCTGAAATATA 148
    ||||||||||||||||||||
Db 120 CTTTAAATAGCTGAAATATA 98
    ||||||||||||||||||||

```

Search Completed: March 17, 2003, 21:29:38
Job time : 1464 secs

•

•

GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 17, 2003, 19:52:45 : Search time 224 seconds

(without alignments) 2372.641 Million cell updates/sec

Title: US-09-247-874c-2_COPY_8710_8945

Perfect score: 236

Sequence: 1 ttgtgattcattgtctctat.....ataacttaactgaagaataa 236

Scoring table: OLIGO_MNC

Gapop 60.0 , Gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : N_Geneseq-101002:*

1: /SIDS2/qcqdta/geneeq/geneeqn-emb1/NA1980.DAT:*

2: /SIDS2/qcqdta/geneeq/geneeqn-emb1/NA1981.DAT:*

3: /SIDS2/qcqdta/geneeq/geneeqn-emb1/NA1982.DAT:*

4: /SIDS2/qcqdta/geneeq/geneeqn-emb1/NA1983.DAT:*

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7: /SIDS2/qcqdta/geneeq/geneeqn-emb1/NA1986.DAT:*

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11: /SIDS2/qcqdta/geneeq/geneeqn-emb1/NA1990.DAT:*

12: /SIDS2/qcqdta/geneeq/geneeqn-emb1/NA1991.DAT:*

13: /SIDS2/qcqdta/geneeq/geneeqn-emb1/NA1992.DAT:*

14: /SIDS2/qcqdta/geneeq/geneeqn-emb1/NA1993.DAT:*

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18: /SIDS2/qcqdta/geneeq/geneeqn-emb1/NA1997.DAT:*

19: /SIDS2/qcqdta/geneeq/geneeqn-emb1/NA1998.DAT:*

20: /SIDS2/qcqdta/geneeq/geneeqn-emb1/NA1999.DAT:*

21: /SIDS2/qcqdta/geneeq/geneeqn-emb1/NA2000.DAT:*

22: /SIDS2/qcqdta/geneeq/geneeqn-emb1/NA2001A.DAT:*

23: /SIDS2/qcqdta/geneeq/geneeqn-emb1/NA2001B.DAT:*

24: /SIDS2/qcqdta/geneeq/geneeqn-emb1/NA2002.DAT:*

Print. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	236	100.0	9721	21	AAA50175 Human interleukin-1
2	194	82.2	656	21	AAA51659 Human interleukin-1-beta
3	194	82.2	1496	21	AAAF20946 Human interleukin-1
4	194	82.2	1496	21	AAA34824 Human adenovirus re
5	194	82.2	1507	6	AAAS0060 Sequence encoding
6	194	82.2	1507	14	AAQ50981 Human interleukin-
7	194	82.2	9721	20	AAK75924 Human interleukin-
8	194	82.2	9721	21	AAAF20945 Human interleukin-
9	194	82.2	9721	21	AAAC63768 Human IL-1B gene.

10	194	82.2	9721	21	AAA50174 Human interleukin-
11	194	82.2	9721	21	AAA34823 Human adenovirus re
12	194	82.2	9721	22	AAAF27666 IL-1B RNA, uniden
13	194	82.2	9721	22	AAAC91434 Human IL-1B nucle
14	194	82.2	9721	24	AAAD5192 Human Proinfertleu
15	194	82.2	29433	21	AAAF20950 Human interleukin-
16	194	82.2	29433	21	AAA34828 Human adenovirus re
17	194	82.2	209273	21	AAAF21477 Human factor-relat
18	189	80.1	1382	24	ABL46348 Human interleukin-
19	189	80.1	1497	21	AAAF20944 Human interleukin-
20	189	80.1	1497	21	AAA44822 Human adenovirus re
21	189	80.1	1497	24	ABK83933 Human cDNA differe
22	189	80.1	7824	16	AAO74052 Human interleukin-
23	189	80.1	7824	24	AAH24368 Human IL1B gene.
24	189	80.1	7824	24	ABK50291 Human interleukin-
25	189	80.1	7824	24	ABK60293 Human interleukin-
26	189	80.1	14690	20	AAK22303 Human IL-1ra BAC c
27	138	58.5	1497	15	AAQ58462 IL-1 beta gene.
28	132	55.9	1514	21	AAZ55973 cDNA encoding huma
29	125	53.0	454	16	AAAT20507 Human gene signal
30	121	51.3	1404	7	AAAB60283 Sequence encoding
31	121	51.3	1404	8	AAAB70505 Sequence encoding
32	121	51.3	1404	14	AAQ51110 Human interleukin-
33	58	24.6	60	24	ABN38537 Human spliced tran
34	44	18.6	44	21	AAAF50182 Probe used to dete
35	44	18.6	44	21	AAAF50184 Probe used to dete
36	41	17.4	1458	11	AAQ05593 Monkey IL-2 beta g
37	33	14.0	8639	20	AAK02995 Human IL-1ra BAC c
38	24	10.2	44	21	AAAF50183 Probe used to dete
39	23	9.7	42	21	AAAF50181 Probe used to dete
40	22	9.3	2983	23	AHL09950 Prosopha melanog
41	21	8.9	21	21	AAAF50179 Primer used to det
42	20	8.5	28	21	AAAF50180 Primer used to det
43	20	8.5	32	21	AAAF50178 Primer used to det
44	19	8.1	579	24	ABQ35866 cDNA encoding ide fo
45	19	8.1	579	24	ABQ35867 cDNA encoding ide fo

ALIGNMENTS

RESULT 1

ID AAA50175 standard: DNA: 9721 bp.

AAA50175

AC AAA50175:

XX 07-NOV-2000 (first entry)

XX

DE Human interleukin-1 beta allele 2 (+6912).

XX

XX Interleukin-1 beta; IL-1B; human; polymorphism; inflammation;

XX coronary artery disease; osteoporosis; nephropathy;

XX alopecia areata; Graves disease; systemic lupus erythematosus;

XX lichen sclerosus; ulcerative colitis; diabetic retinopathy;

XX periodontal disease; juvenile chronic arthritis; psoriasis;

XX insulin dependent diabetes; asthma; lung fibrosis;

XX chronic inflammatory liver disease; rheumatoid arthritis;

XX chronic inflammatory lung disease; antiinflammatory; osteoporosis;

XX dermatological; immunosuppressive; antidiabetic; antithyroid;

XX antihistatic; antirheumatic; antitussive; antipruritic;

XX hepatotropic; antitumor; diagnosis; therapy; ds.

XX

OS Homo sapiens.

XX

XX Key location/Qualifiers

XX variation replace(8904,c)

XX FT /tag= 2

XX FT /note= "IL-1B allele 2 (+6912)"

XX

XX WO200047619-A1.

XX

XX 17-AUG-2000.

|||||
Db 549 AAGTCCTTTAAATTAACACGCAAAATATATAACGTCAGATTATTAAATGCAATATTAT 608
QY 181 AATGAGCAAAATAT 194
Db 609 AATGAGCAAAATAT 622
RESULT 3
AAF20946
10 AAF20946 standard; DNA: 1496 BP.
XX
XX AAF20946:
XX
XX 14-MAR-2001 (first entry)
XX
XX Human interleukin-1 polynucleotide fragment #2513.
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX human; airway disorder; bronchoconstriction; lung inflammation;
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;
XX immunosuppressive; antisthmatic; analgesic; hypotensive; cytoskeletal;
XX respiratory obstruction; pulmonary obstruction; impeded respiration;
XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
XX pulmonary hypertension; emphysema; pulmonary transplantation rejection;
XX chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
XX cancer; SS.
XX
XX Homo sapiens.
XX
XX W0200062736-A2.
XX
XX 26-OCT-2000.
XX
XX 24-MAR-2000; 2000WO-0508020.
XX
XX 06-APR-1999; 99US-0127958.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX (NYCE/) NYCE J W.
XX
XX Nyce JW:
XX
XX WPI: 2000-679539/66.
XX
XX Low adenosine (A) content antisense oligonucleotides which do not
XX trigger adenosine receptors during metabolism, useful e.g. for treating
XX cancers and respiratory obstructions -
XX
XX Disclosure: Page 232-233; 1592pp; English.
XX
XX The present invention describes low adenosine (A) content antisense
XX oligonucleotides and compositions (I) comprising them. In the antisense
XX oligonucleotides the A is replaced by a 'universal' or alternative base.
XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
XX immunosuppressive, antisthmatic, hypotensive and cytoskeletal activities.
XX The antisense oligonucleotides and (I) can be used to down-regulate the
XX expression and or activity of target polypeptides associated with
XX lung/respiratory disorders and malignancies, such as stimulating and
XX activating peptide factors and transmitters, transcription factors,
XX immunoglobulins and antibodies, antibody receptors, cytokines and
XX chemokines, endogenously produced specific and non-specific enzymes,
XX binding proteins, adhesion molecules and their receptors, cytokine and
XX chemokine receptors, adenosine receptors, bradykinin receptors, central
XX nervous system (CNS) and peripheral nervous and non-nervous system
XX receptors, CNS and peripheral nervous and non-nervous system peptide
XX transmitters, defensins, growth factors, vasoactive peptides and
XX receptors, binding proteins and malignancy associated proteins. The
XX antisense oligonucleotides may be used in this way to treat disorders
XX including respiratory obstruction (especially pulmonary obstruction
XX and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
XX and/or surfactant hypoproduction which are associated with a disease or

CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergic, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
XX Sequence 1496 BP; 416 A; 361 C; 328 G; 391 T; 0 other:
S0
Query Match 82.2%; Score 194; DF 21; Length 1496;
Best Local Similarity 100.0%; Pred. No. 1,3e-85;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTGATTCATTCGCTAATATTATTCGAAAGGGGCGAGAGTACGATGCTGTAAAGCA 60
Db 1269 TTTGATTCATTCGCTAATATTATTCGAAAGGGGCGAGAGTACGATGCTGTAAAGCA 1328
QY 61 GCGTACGTTTAAATAGCTATGCAATTCGATTTGAGCTGCTGCTTAAATC 120
Db 1329 GCGTACGTTTAAATAGCTATGCAATTCGATTTGAGCTGCTGCTTAAATC 1388
QY 121 AAGTCCTTTAAATTAAGACTGAAATATATAAAGCTCAGATTTAAATGCAATATTAT 180
Db 1389 AAGTCCTTTAAATTAAGACTGAAATATATAAAGCTCAGATTTAAATGCAATATTAT 1448
QY 181 AATGAGCAAAATAT 194
Db 1449 AATGAGCAAAATAT 1462
RESULT 4
AAA34824
ID AAA34824 standard; DNA: 1496 BP.
XX
XX AAA34824:
XX
XX 28-JUL-2000 (first entry)
XX
XX Human adenosine receptor related polynucleotide SEQ ID NO:2513.
XX
XX
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphorothioate; impaired respiration; inflammation; allergy;
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX antiallergic; antisthmatic; cytoskeletal; analgesic; impaired airway;
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX cancer; leukaemia; lymphoma; carcinoma; metastasis; SS.
XX
XX Homo sapiens.
XX
XX W0200009525-A2.
XX
XX 24-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17712.
XX
XX 03-AUG-1998; 98US-0095212.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW:
XX
XX WPI: 2000-205971/18.
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
XX vasoconstriction, inflammation, allergies, asthma, hypertension,
XX bronchitis, emphysema, respiratory distress syndrome, ischemia or
XX cancers -
XX
XX Disclosure: Page 675; 1343pp; English.

XX The present invention describes a new composition comprising an
 CC antihemophilic acid (AH) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The AH can have anti-inflammatory, analgesic,
 CC antispasmodic, cytosolic and analgesic activities. The composition
 CC is useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects affect the lungs of a subject. They can be used for treating
 CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC the AH reduces side effects. The A-containing AHs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32413 to AAA35412 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680
 CC (AAA12323 to AAA39942) are specifically claimed AHs from the present
 CC invention. N.B. Sequences given in the disclosure of the present
 CC invention do not match up with their corresponding SEQ ID NO: sequences
 CC given in the sequence listing.

XX Sequence 1496 BP: 416 A; 361 C; 328 G; 391 T; 0 other:

XX Query Match 82.2%; Score 194; DB 21; Length 1496;

XX Best Local Similarity 100.0%; Pred. No. 1,46-85;

XX Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 TTTTGATTCATGGCTGCTAATTTATTCAGAGGCGGAGAGTACGCTGCTTAAGA 60
 DB 1269 TTTTATTCATGGCTGCTAATTTATTCAGAGGCGGAGAGTACGCTGCTTAAGA 1328
 YY 61 GCTTACCTTTTAAATGATGATGATTAATTCATTCGACGCTGCTGCTTTAATTC 120
 DB 1329 GCTTACCTTTTAAATGATGATGATTAATTCATTCGACGCTGCTGCTTTAATTC 1388
 YY 121 AAGTCTTTTAAATGATGATGATTAATTCATTCGACGCTGCTGCTTTAATTC 180
 DB 1389 AAGTCTTTTAAATGATGATGATTAATTCATTCGACGCTGCTGCTTTAATTC 1448
 YY 181 AAGTCTTTTAAATGATGATGATTAATTCATTCGACGCTGCTGCTTTAATTC 194
 DB 1449 AAGTCTTTTAAATGATGATGATTAATTCATTCGACGCTGCTGCTTTAATTC 1462

DB 1449 AAGTCTTTTAAATGATGATGATTAATTCATTCGACGCTGCTGCTTTAATTC 1462

RESULT 5
 ID AAN50060 standard; cDNA: 1507 BP.

XX AAN50060;

XX 09-SBP-1991 (first entry)

XX Sequence encoding interleukin-1 (IL-1).

XX Immunological reagent: T cell stimulant; B cell; immunoglobulin; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 87..894

XX E316.1901 A.

XX Z1-087-1985.

XX 07-MAY-1985; 85EP 0304234.

XX 11-FEB-1985; 85OS-0700374.

XX (NME) NEW ENGLAND MED GEN.

XX Auten PE, Webb AC, Gohke L, DiMartino CA, Rosengasser L, Rich A;

XX Wolf SM;

XX WPI: 1985-291135/47.

XX P-OSDH: AAN50043.

XX Recombinant cloning vehicle contg. human interleukin 7 gene or its

XX fragments, producing new biologically active polypeptide(s)

XX Claim 7: page 34-35; 39pp; Eng158b.

XX A pure cDNA of 1507 bp (AAN50060) (and its 1-606, 1-677, 1455, 1507;

XX 482-1501; 482-677; and 1455-1507 fragments) are claimed. Also

XX claimed is a recombinant DNA cloning vehicle contg. the human IL-1

XX gene sequence. Specifically the vehicle contains the sequence coding

XX for the new 287 AA sequence (AAN50043) or the following new fragments

XX (1) 9-224; (2) 1-210-X; (3) 144-287; and (4) 144-210-(X); (X=Asn

XX Ser-Thr-Trp-Gly-Val-Ileu Ser-Leu Asn-Gln-Val-Ileu).

XX Sequence 1507 BP: 427 A; 361 C; 328 G; 391 T; 0 other:

XX Query Match 82.2%; Score 194; DB 6; Length 1507;

XX Best Local Similarity 100.0%; Pred. No. 1,46-85;

XX Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 TTTTGATTCATGGCTGCTAATTTATTCAGAGGCGGAGAGTACGCTGCTTAAGA 60
 DB 1269 TTTTATTCATGGCTGCTAATTTATTCAGAGGCGGAGAGTACGCTGCTTAAGA 1328
 YY 61 GCTTACCTTTTAAATGATGATGATTAATTCATTCGACGCTGCTGCTTTAATTC 120
 DB 1329 GCTTACCTTTTAAATGATGATGATTAATTCATTCGACGCTGCTGCTTTAATTC 1388
 YY 121 AAGTCTTTTAAATGATGATGATTAATTCATTCGACGCTGCTGCTTTAATTC 180
 DB 1389 AAGTCTTTTAAATGATGATGATTAATTCATTCGACGCTGCTGCTTTAATTC 1448
 YY 181 AAGTCTTTTAAATGATGATGATTAATTCATTCGACGCTGCTGCTTTAATTC 194
 DB 1449 AAGTCTTTTAAATGATGATGATTAATTCATTCGACGCTGCTGCTTTAATTC 1462

DB 1449 AAGTCTTTTAAATGATGATGATTAATTCATTCGACGCTGCTGCTTTAATTC 1462

RESULT 6
 ID AAN50981 standard; cDNA: 1507 BP.

XX AAN50981;

XX 19-MAY-1994 (first entry)

XX human interleukin 1 coding sequence.

XX hIL-1; interleukin; cytokine; truncated; N-terminal deletion;

XX C-terminal deletion; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 87..896

XX E316.1901 A.

XX Z1-087-1985.

XX 07-MAY-1985; 85EP 0304234.

XX 18-NOV-1994.


```
XX 07-MAY-1985: 85EP-0303234.
XX 18-MAY-1984: 84US-0611669.
XX 11-FEB-1985: 85US-0700374.
XX (MAST) MASSACHUSETTS INST TECHNOLOGY.
XX (NEW-) NEW ENGLAND MED. CENT HOSPITALS.
XX (TUFT) TUFTS COLLEGE.
XX (WELL-) WELLESLEY COLLEGE.
XX Atron PE, Dinarello CA, Gehlke L, Rich A, Rosenwasser LJ;
XX Webb AC, Wolff SM;
XX WPI: 1993-360975/46.
XX F-PSDB: AAR42213.
XX New DNA encoding protein with IL-1 activity - useful in
XX monitoring disease states e.g. cancer and studying inflammation
XX e.g. in arthritis etc.
XX Claim 1: Page 11-16: 24pp: English.
XX DNA comprising part of the nucleotide sequence AA050981 which encodes
XX a polypeptide having IL-1 activity and a mol.wt. of 20000 is claimed.
XX Specifically, the region between nucleotides 111-717 has been found
XX to retain IL-1 activity (see AA045464).
XX Sequence 1507 BP: 427 A; 361 C; 328 G; 394 T; 0 other;
XX Query Match 82.2%; Score 194; DB 14; Length 1507;
XX Best local Similarity 100.0%; Pred. No. 1.3e-85;
XX Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 TTTGATTCATTCGCTTAATTATTCGAAGGGGCAAGAGTACGCTGCTGTAAAGA 60
XX 1269 TTTGATTCATTCGCTTAATTATTCGAAGGGGCAAGAGTACGCTGCTGTAAAGA 1328
XX 61 GCCTAGTTTAAATAGCTATGAGTCAATTCATTGGAGCTGTGCTCTTTAAATC 120
XX 1329 GCCTAGTTTAAATAGCTATGAGTCAATTCATTGGAGCTGTGCTCTTTAAATC 1388
XX 121 AAGCTCTTAAATAGCTATGAGTCAATTCATTGGAGCTGTGCTCTTTAAATC 180
XX Db 1389 AAGCTCTTAAATAGCTATGAGTCAATTCATTGGAGCTGTGCTCTTTAAATC 1448
XX QY 181 AATGAGCAAAATAT 194
XX 1449 AATGAGCAAAATAT 1462
XX
XX RESULT 7
XX AAX75924
XX ID AAX75924 standard; DNA: 9721 BP.
XX AC AAX75924.
XX
XX 29-JUL-1999 (first entry)
XX Human interleukin 1A gene.
XX DE Human interleukin 1A gene.
XX KM Human; interleukin 1; IL-1A; IL-1A; IL-1A; diagnosis; detection;
XX chronic obstructive airway disease; chronic bronchitis; emphysema;
XX asthma; chronic bronchitis; proinflammatory phenotype; ss.
XX OS Homo sapiens.
XX PN W09924615-A2.
XX 20-MAY-1999.
XX 09-NOV-1998: 98WO-0523721.
XX
```

```
PR 12-JAN-1998: 98US-0005923.
PR 07-NOV-1997: 97GB-0023553.
XX (MEDI-) MEDICAL SCI SYSTEMS INC.
XX Barnes PJ, Duff GW, Giovine M, Lim S;
XX WPI: 1999-327420/27.
XX Genotyping nucleic acid samples for interleukin-1 (IL-1)
XX proinflammatory haplotype alleles, useful for predicting
XX susceptibility to developing chronic obstructive airway disease
XX Example 1: Fig 2: 37pp: English.
XX The present invention describes genotyping a nucleic acid sample from a
XX subject to determine at least one allele of an interleukin-1 (IL-1)
XX proinflammatory haplotype. A method has also been described for
XX determining a subject's susceptibility to developing chronic obstructive
XX airway disease (COAD) or for predicting the rapidly or ultimate
XX progression of a COAD in the subject by: (a) obtaining a nucleic acid
XX sample from the subject; and (b) detecting at least one allele of an
XX IL-1 proinflammatory haplotype in the sample, where detection of at
XX least one of these alleles indicates that the patient has an increased
XX susceptibility to developing COAD. The method is useful for determining
XX the susceptibility of subjects to developing chronic obstructive airway
XX disease or for predicting the rapidly or ultimate progression of
XX chronic obstructive airway disease (COAD). COAD can be asthma, emphysema,
XX chronic bronchitis or chronic obstructive airway disease (COAD).
XX early identification of chronic obstructive airway disease (COAD),
XX facilitating administration of appropriate treatment at the earliest
XX stage, thereby increasing the probability of a positive outcome. The
XX present sequence represents the human IL-1B gene.
XX Sequence 9721 BP: 2662 A; 2128 C; 2121 G; 2608 T; 2 other;
XX Query Match 82.2%; Score 194; DB 20; Length 9721;
XX Best local Similarity 100.0%; Pred. No. 1.3e-85;
XX Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 TTTGATTCATTCGCTTAATTATTCGAAGGGGCAAGAGTACGCTGCTGTAAAGA 60
XX Db 8710 TTTGATTCATTCGCTTAATTATTCGAAGGGGCAAGAGTACGCTGCTGTAAAGA 8769
XX QY 61 GCCTAGTTTAAATAGCTATGAGTCAATTCATTGGAGCTGTGCTCTTTAAATC 120
XX Db 8770 GCCTAGTTTAAATAGCTATGAGTCAATTCATTGGAGCTGTGCTCTTTAAATC 8829
XX QY 121 AAGCTCTTAAATAGCTATGAGTCAATTCATTGGAGCTGTGCTCTTTAAATC 180
XX Db 8830 AAGCTCTTAAATAGCTATGAGTCAATTCATTGGAGCTGTGCTCTTTAAATC 8889
XX QY 181 AATGAGCAAAATAT 194
XX Db 8890 AATGAGCAAAATAT 8903
XX
XX RESULT 8
XX AAF20945
XX ID AAF20945 standard; DNA: 9721 BP.
XX AC AAF20945.
XX
XX 14-MAR-2001 (first entry)
XX Human interleukin-1 polynucleotide fragment #2512.
XX DE Human interleukin-1 polynucleotide fragment #2512.
XX KM low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX human; airway disorder; bronchoconstriction; lung inflammation;
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;
XX immunosuppressive; antiallergic; analgesic; hypotensive; cytostatic;
XX respiratory obstruction; pulmonary obstruction; impeded respiration;
XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
XX
```


QY 121 AAGTCCTTATTAGACGTGAAATATATAGCTCAGATTATTAAATGGCAATTATTAT 180
 |||
 DB 8830 AAGTCCTTATTAGACGTGAAATATATAGCTCAGATTATTAAATGGCAATTATTAT 8889
 QY 181 AATGAGCAATAT 194
 |||
 DB 8890 AATGAGCAATAT 8903
 RESULT 10
 AAA50174
 ID AAA50174 standard; DNA: 9721 BP.
 XX AAA50174;
 AC
 XX
 DT 07-NOV 2000 (first entry)
 XX
 DE Human Interleukin-1 beta allele 1 (+6912).
 XX
 KW Interleukin-1 beta; IL-1b; human; polymorphism; inflammation;
 KW coronary artery disease; osteoporosis; nephropathy;
 KW alopecia areata; Graves disease; systemic lupus erythematosus;
 KW lichen sclerosus; ulcerative colitis; diabetic retinopathy;
 KW periodontal disease; juvenile chronic arthritis; psoriasis;
 KW insulin dependent diabetes; asthma; lung fibrosis;
 KW chronic inflammatory liver disease; rheumatoid arthritis;
 KW chronic inflammatory lung disease; antiinflammatory;
 KW dermatological; immunosuppressive; antidiabetic; antihypertoid;
 KW arthritic; antirheumatic; antiasthmatic; antipsoriatic;
 KW hepatotropic; anticancer; diagnosis; therapy; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT variation replace(8904,G)
 FT /tag - a
 FT /note- "IL-1b allele 1 (+6912)"
 PN W0200047619-A1.
 PD 17-AUG-2000.
 XX
 PF 10-FEB-2000; 2000MO-0503443.
 XX
 PR 10-FEB-1999; 99US-0247874.
 XX
 PA (INT-) INTERLEUKIN GENETICS INC.
 XX
 PI Duff GW, Di Giovine FS;
 XX
 DR WPI: 2000-558192/51.
 XX
 PT Novel methods and nucleic acids for diagnosing and treating disorders
 PT associated with high levels of Interleukin beta, especially
 PT inflammatory diseases -
 PS
 PS Disclosure: Fig 1; 74pp; English.
 XX
 CC The present sequence is that of human interleukin-1 beta (IL-1b)
 CC allele 1 (+6912), which is a form of the IL-1b gene that contains
 CC cytosine at position +6912; IL-1b allele 2 (+6912) has guanine at
 CC this position (see AAA50175). The invention is based on the
 CC identification of this novel allele at marker +6912 of the IL-1b
 CC gene. The C to G transition occurs within the 3' untranslated
 CC region of the IL-1b gene and results in an increased level of IL-1b
 CC protein. Individuals homozygous for the IL-1b allele 2 (+6912)
 CC accumulate approximately 4 times more immunoreactive IL-1b protein
 CC than homozygotes for IL-1b allele 1 (+6912). Methods and kits are
 CC provided for detecting IL-1b allele 2 (+6912), or an allele in
 CC linkage disequilibrium with an IL-1b allele 2 (+6912), and
 CC thereby determining a patient's susceptibility to developing
 CC inflammatory disorders, especially coronary artery disease.

CC osteoporosis, nephropathy in diabetes mellitus, alopecia areata,
 CC Graves disease, systemic lupus erythematosus, lichen sclerosus,
 CC ulcerative colitis, diabetic retinopathy, periodontal disease,
 CC juvenile chronic arthritis, psoriasis, insulin dependent diabetes,
 CC asthma, chronic inflammatory liver disease, chronic inflammatory
 CC lung disease, lung fibrosis, and rheumatoid arthritis (claimed).
 CC Identification of the IL-1b allele 2 (+6912) and its involvement in
 CC IL-1b overproduction also enables screening assays for identifying
 CC IL-1b antagonists that can be used to treat conditions associated
 CC with IL-1b allele 2 (+6912). Transgenic animals are also claimed,
 CC and can be used to identify IL-1b agonists and antagonists, or
 CC to confirm the safety and efficacy of candidate therapeutics.
 XX
 SO Sequence 9721 BP; 2661 A; 2122 G; 2608 T; 2 other:
 Query Match 82.2%; Score 194; DB 21; Length 9721;
 Best local Similarity 100.0%; Pred. No. 1,36-85;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTGATTCATGCTCAATTTATTCAGAGGAGGAAAGATAGCATCTCTGTAAGAA 60
 |||
 DB 8710 TTTTGATTCATGCTCAATTTATTCAGAGGAGGAGATAGCATCTCTGTAAGAA 8769
 QY 61 GCCTAGTTTATFAGCAATGATCAATTCATTTGGACTAGTGTCTCTTTAAATC 120
 |||
 DB 8770 GCCTAGTTTATFAGCAATGATCAATTCATTTGGACTAGTGTCTCTTTAAATC 8829
 QY 121 AAGTCCTTATTAGACGTGAAATATATAGCTCAGATTATTAAATGGCAATATTAT 180
 |||
 DB 8830 AAGTCCTTATTAGACGTGAAATATATAGCTCAGATTATTAAATGGCAATATTAT 8889
 QY 181 AATGAGCAATAT 194
 |||
 DB 8890 AATGAGCAATAT 8903
 RESULT 11
 AAA34823
 ID AAA34823 standard; DNA: 9721 BP.
 XX AAA34823;
 AC
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SHU 10 N1:2512.
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200009525-A2.
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99MO-US17712.
 XX
 PR 03-AUG-1998; 98US-0095212.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 DR WPI: 2000-205971/18.
 XX
 PT Now antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,

XX 24-MAY-2000: 2000WO-US14299.
 XX
 PF 24-MAY-1999: 990S-0317674.
 XX
 PR 01-NOV-1999: 990S-041352.
 XX
 XX (INTE-) INTERLEUKIN GENETICS INC.
 PA
 XX Korman KS, Duff GW, Crossman DC, Francis SE, Stephenson K;
 PI
 XX WPI: 2001-025173/03.
 DR
 XX
 XX
 PT Diagnosing or determining susceptibility to developing restenosis
 PT involves detecting restenosis associated allele in a nucleic acid
 PT sample.
 XX
 XX
 PS Disclosure: Fig 2; 129pp: English.
 XX
 CC The present sequence is given in a specification relating to a method for
 CC determining whether a subject has or is predisposed to developing an
 CC arterial restenosis. The method comprises detecting a restenosis
 CC associated allele (RAA) in a nucleic acid sample from the subject, where
 CC detection of the RAA indicates that the subject has or is predisposed to
 CC the development of a restenosis. The restenosis associated allele
 CC pattern permits the diagnosis of occlusive cardiovascular disorder. The
 CC diagnosis allows the most suitable treatment methods for restenosis to be
 CC used e.g. selecting therapies for initial vascular stenosis most likely
 CC to avoid subsequent stenoses. The detection methods identify restenosis
 CC therapeutics, agonists and antagonists, (proteins, peptides,
 CC peptidomimetics, small molecules or nucleic acids, e.g. anti-sense,
 CC ribozyme and triplex nucleic acids) which are used to treat restenosis.
 XX
 SQ Sequence 9721 BP: 2661 A: 2328 C: 2122 G: 2608 T: 2 other:

Query Match 82.2%; Score 194; DB 22; Length 9721;
 Best Local Similarity 100.0%; Pred. No. 1.3e-85;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTATTCATTCGCTAATTATTCGAAGGGGCGACAGACAGTGTCTGTAAGA 60
 DB 8710 TTTTATTCATTCGCTAATTATTCGAAGGGGCGACAGACAGTGTCTGTAAGA 8769
 QY 61 GCTTACGTTTTTAATAGCTATGACATCAATTCATTGCGCTGCTCTTTAAATC 120
 DB 8770 GCGTACGTTTTTAATAGCTATGACATCAATTCATTGCGCTGCTCTTTAAATC 8829
 QY 121 AAGTCTTTAATTAAGACTGCAAAATATATAGCTAGATTATTTAAATGGAATATTAT 180
 DB 8830 AAGTCTTTAATTAAGACTGCAAAATATATAGCTAGATTATTTAAATGGAATATTAT 8889
 QY 181 AAATGAGTCAATAT 194
 DB 8890 AAATGAGTCAATAT 8903

RESULT 14
 AAF35192
 ID AAF35192 standard: DNA: 9721 BP.
 XX
 AC AAF35192;
 XX
 DT 25-JUL-2002 (first entry)
 DE
 XX Human prointerleukin-1 beta (IL-1 beta) gene.
 XX
 KW Unexplained recurrent pregnancy loss; immunologic reproductive failure;
 KW URP; prointerleukin-1beta; IL-1beta; human; ds.
 XX
 OS Homo sapiens.
 KW
 PN W0200222877 A2.
 XX
 PD 21-MAR-2002.

XX 12-SEP-2001: 2001WO-US28465.
 PE
 XX 12-SEP-2000: 2000US-241785P.
 XX
 XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 PA (DAND) DANA FARBER CANCER INST INC.
 XX
 PI Hill JA, Wang YC, Anderson DJ, Yunis EJ;
 DR
 XX WPI: 2002-362362/39.
 XX
 XX
 PT Evaluating risk of unexplained recurrent pregnancy loss in a subject,
 PT by testing presence of a variant in interleukin-1 beta promoter region
 PT and/or in CD46 gene intron 1 region in a sample obtained from the
 PT subject.
 XX
 XX
 PS Example 2 and 3; Page 51-54; 57pp: English.
 XX
 CC The invention relates to a method for evaluating and treating risk of
 CC unexplained recurrent pregnancy loss (URPL) in a subject suspected of
 CC having immunologic reproductive failure. The method involves testing a
 CC sample obtained from the subject for the presence of a variant in the
 CC human interleukin-1beta (IL-1beta) promoter region, and/or a variant
 CC in the CD46 gene intron 1 region, where the presence of the variant,
 CC indicates an elevated risk of developing recurrent pregnancy loss.
 CC The present sequence is human prointerleukin-1 beta (IL-1 beta) gene.
 XX
 SQ Sequence 9721 BP: 2661 A: 2328 C: 2122 G: 2608 T: 2 other:

Query Match 82.2%; Score 194; DB 24; Length 9721;
 Best Local Similarity 100.0%; Pred. No. 1.3e-85;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTATTCATTCGCTAATTATTCGAAGGGGCGACAGACAGTGTCTGTAAGA 60
 DB 8710 TTTTATTCATTCGCTAATTATTCGAAGGGGCGACAGACAGTGTCTGTAAGA 8769
 QY 61 GCTTACGTTTTTAATAGCTATGACATCAATTCATTGCGCTGCTCTTTAAATC 120
 DB 8770 GCGTACGTTTTTAATAGCTATGACATCAATTCATTGCGCTGCTCTTTAAATC 8829
 QY 121 AAGTCTTTAATTAAGACTGCAAAATATATAGCTAGATTATTTAAATGGAATATTAT 180
 DB 8830 AAGTCTTTAATTAAGACTGCAAAATATATAGCTAGATTATTTAAATGGAATATTAT 8889
 QY 181 AAATGAGTCAATAT 194
 DB 8890 AAATGAGTCAATAT 8903

RESULT 15
 AAF20950
 ID AAF20950 standard: DNA: 29433 BP.
 XX
 AC AAF20950;
 XX
 DT 14-MAR-2001 (first entry)
 DE
 XX Human interleukin-1 polynucleotide fragment #2517.
 XX
 KW Low adenovine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilation; antiinflammatory;
 KW immunosuppressive; antiallergic; hypotensive; cyclostatic;
 KW respiratory obstruction; pulmonary; hypoxia; hypoxemia; hypoxia;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; ROS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.

Search completed: March 17, 2003, 20:40:15
 Job time : 257 secs

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XX  W020006.2756 A2.
FN
XX  26-087-2000.
FD
XX  24 MAR 2000; 2000WD-0508020.
FE
XX  06-APR-1999; 9908-0127958.
FR
XX  (OYB*) UNIV EASI CAROLINA.
PA  (NRCF) NRCF J.W.
XX
XX  Nycro J.W.
XX  W01; 2000 6/79549/56.
XX
XX  low adenosine (A) content antisense oligonucleotides which do not
XX  trigger adenosine receptors during metabolism, useful e.g. for treating
XX  cancers and respiratory obstructions.
XX
XX  [abstract; Page 221-227; 1592pp; English].
XX
XX  The present invention describes low adenosine (A) content antisense
XX  oligonucleotides and compositions (1) comprising them. In the antisense
XX  oligonucleotides the A is replaced by a "universal" or alternative base.
XX  (1) can have respiratory, bronchodilator, antihistaminic, anesthetic,
XX  immunosuppressive, antitumor, hypotensive and cytostatic activities.
XX  The antisense oligonucleotides and (1) can be used to down-regulate the
XX  expression and/or activity of target polypeptides associated with
XX  lung/respiratory disorders and malignancies, such as stimulating and
XX  activating peptide factors and transmitters, transcription factors,
XX  immunoglobulins and antibodies, antibody receptors, cytokines and
XX  chemokines, endogenously produced specific and non-specific enzymes,
XX  binding proteins, adhesion molecules and their receptors, cytokine and
XX  chemokine receptors, adenosine receptors, bradykinin receptors, central
XX  nervous system (CNS) and peripheral nervous and non-nervous system
XX  receptors, CNS and peripheral nervous and non-nervous system peptide
XX  transmitters, defensins, growth factors, vasoactive peptides and
XX  receptors, binding proteins and malignancy associated proteins. The
XX  antisense oligonucleotides may be used in this way to treat disorders
XX  including respiratory obstruction (especially pulmonary obstruction
XX  and/or bronchoconstriction) and/or lung inflammation, allergy (es)
XX  and/or surfactant hypoproduction which are associated with a disease or
XX  condition selected from pulmonary vasoconstriction, inflammation,
XX  allergies, asthma, impaired respiration, respiratory distress syndrome
XX  (ARDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
XX  hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
XX  pulmonary transplantation rejection, pulmonary infections, bronchitis,
XX  and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
XX  fragments and antisense oligonucleotides used in the exemplification of
XX  the present invention.
XX
XX  Sequence 29433 BP; 8714 A; 6519 G; 5920 C; 8278 T; 2 other;

```

Query Match: 82.28; Score 194; DB 21; Length 29433;
 best local similarity 100.0%; Prod. No. 1.2e-85;
 Mismatches 194; conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY  1 TTTGATTCATGCTCTAATTTATTCAAAGAGGAGAAATACACATGCTCTAAAGA 60
   |||||
DB  22177 TTTGATTCATGCTCTAATTTATTCAAAGAGGAGAAATACACATGCTCTAAAGA 22236
QY  61 GCTTACGTTTAAATGATGAGATTAATTCATTTGACATGCTGCTCTTTAAATC 120
   |||||
DB  22247 GCTTACGTTTAAATGATGAGATTAATTCATTTGACATGCTGCTCTTTAAATC 22296
QY  121 AACTCTTTAATTAAGCTGAAAAATATTAAGTCAAGATTATTTAAATGCAATATTTAT 180
   |||||
DB  22297 AACTCTTTAATTAAGCTGAAAAATATTAAGTCAAGATTATTTAAATGCAATATTTAT 22356
QY  181 AAATGACGAAATAT 194
   |||||
DB  22457 AAATGACGAAATAT 22470

```

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olnucleic - nucleic search, using sw model

Run on: March 17, 2003, 20:32:30 ; Search time 1145 Seconds

(without alignments)
5998.482 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

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2: gb_bt:*
3: gb_in:*
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7: gb_ph:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: gb_vl:*
16: em_ba:*
17: em_bt:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pa:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_bt:*
31: em_bt:*
32: em_bt:*
33: em_bt:*
34: em_bt:*
35: em_bt:*
36: em_bt:*
37: em_bt:*
38: em_bt:*
39: em_bt:*
40: em_bt:*
41: em_bt:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	194	82.2	614	11	G10509
2	194	82.2	656	6	AX027920
3	194	82.2	1466	9	101156
4	194	82.2	1466	9	HMM11
5	194	82.2	1466	9	HMM11
6	194	82.2	1507	6	E00846
7	194	82.2	1507	6	E07942
8	194	82.2	1507	6	AX052806
9	194	82.2	9721	6	AX067266
10	194	82.2	9721	6	AX069435
11	194	82.2	9721	9	HST1LB
12	189	80.1	1382	6	AX019978
13	189	80.1	1473	9	HSPK011B
14	189	80.1	1497	6	AR030386
15	189	80.1	1497	6	E06774
16	189	80.1	1497	9	HMM11BA
17	189	80.1	1522	9	BC008678
18	189	80.1	7824	9	HMM11B
19	189	80.1	17447	9	AV137079
20	189	80.1	154214	9	AC079753
21	132	55.9	1514	6	AR086959
22	132	55.9	1514	6	I00729
23	121	51.3	1404	6	A21148
24	121	51.3	1404	6	E01230
25	121	51.3	1404	6	E11934
26	121	51.3	1404	6	E12090
27	121	51.3	1404	6	E12090
28	41	17.4	1458	6	E02498
29	30	12.7	400	11	G13631
30	22	9.3	1377	4	RAB11B
31	22	9.3	1403	4	RAB11B2
32	22	9.3	23104	2	AC017874
33	22	9.3	171226	3	AC008144
34	22	9.3	238245	3	AF003737
35	21	8.9	150955	2	AC117259
36	21	8.9	155020	2	AC106390
37	20	8.5	56870	9	AL512822
38	20	8.5	59728	2	AC104292
39	20	8.5	70849	2	AC090139
40	20	8.5	91242	9	AP001252
41	20	8.5	105495	9	AC105999
42	20	8.5	105496	9	AF165142
43	20	8.5	120038	9	AC020551
44	20	8.5	126117	2	AL157949
45	20	8.5	140409	2	AC044825

ALIGNMENTS

RESULT 1

G10509

LOCUS human STS CHLC.UTR.00699_X04500.P37183 clone UTR.00699_X04500.

DEFINITION sequence tagged site.

ACCESSION G10509.1 GI:942358

VERSION STS: STS sequence; primer: sequence tagged site.

KEYWORDS Homo sapiens vector-pUC1 host-E.coli dut-ung- (bait) Marker

SOURCE Selected genomic DNA prepared from XY individual of French nationality.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 614)

Prod. No. is the number of results predicted by chance to have a

AUTHORS Murray, J., Sheffield, V., Weber, J.L., Day, G., and Buelow, K.H.
TITLE Cooperative Human Linkage Center
JOURNAL Unpublished (1993)
SYNOPSIS DFR_00699_X04500, CHAC_DFR_00699_X04500_T36097
CONTACT Dr. Jeffrey C. Murray
MAIL The University of Iowa
 Department of Pediatrics, Iowa City, IA 52242, USA
 Tel: (319) 356-3508
 Fax: (319) 356-3447
 Email: jef-murray@uiowa.edu

PRIMER A: AGTCAGATCTCTCCCTTCAGG
PRIMER B: CTGCGCCCTTCGAAATTAAT
STS SIZE: 229
PCR PROFILE:

denaturation: 30 seconds at 94 degrees C
 annealing: 75 seconds at 55 degrees C
 extension: 15 seconds at 72 degrees C
 PCR cycles: 27
 extension: 6 minutes at 72 degrees C

template: 30ng genomic DNA
 primer: each 1.5 pmole
 dNTPs: each 200 uM
 Taq polymerase: 0.3 units
 total vol: 10 uL

Mgt 12: 1.5mM
 KCl: 50mM
 Tris: 10mM
 pH: 8.3

Notes:

Prepared with primer pairs derived from X04500.
 Location/Qualifiers

FEATURES
 source
 1..614
 /organism "Homo sapiens"
 /db_xref "taxon:9606"
 STS
 primer_bind
 complement (189..408)
 base_count 174 a 136 c 120 g 184 t
 origin

Query Match 82.2% Score 194; DB 1; Length 614;
 Host Local Similarity 100.0%; Pred. No. 1.9e-86;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 TTTGATTTATGGTCTAATTTTCAGAGGGGCAAGAGTAGCAGTCTGTAAAGA 60
 |||||||
 DB 371 TTTGATTTATGGTCTAATTTTCAGAGGGGCAAGAGTAGCAGTCTGTAAAGA 430
 UY 61 GCTTACTTTTAAAGCTATGTAATCAATTCAGTTCGTCGTCTTTAAATC 120
 |||||||
 DB 441 GCTTACTTTTAAAGCTATGTAATCAATTCAGTTCGTCGTCTTTAAATC 490
 UY 121 AATGCTTTAATTAAGCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
 |||||||
 DB 491 AATGCTTTAATTAAGCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 550
 UY 181 AATGCTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 194
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 DB 551 AATGCTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 564

RESULT 2
 AX027920
 DEFINITION Sequence 5 from Patient W00093414.
 ACCESSION AX027920
 VERSION AX027920.1 GI:10188746
 KEYWORDS

SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 656)
AUTHORS Kastelic, T. and Cheneval, D.
TITLE Assay for identifying compounds which affect stability of mRNA
JOURNAL Patient: WO 0093414-A 5 06-101-2000;
 KASTELIC, TANIA (CA) ; CHENEVAL, DOMINIQUE (CA) ; NOVATION
 PHARMACEUTICALS, INC (CA)

FEATURES
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 1..656
 /organism "Homo sapiens"
 /db_xref "taxon:9606"
BASE COUNT 176 a 151 c 129 g 200 t
ORIGIN

Query Match 82.2% Score 194; DB 6; Length 656;
 Host Local Similarity 100.0%; Pred. No. 1.9e-86;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 TTTGATTTATGGTCTAATTTTCAGAGGGGCAAGAGTAGCAGTCTGTAAAGA 60
 |||||||
 DB 429 TTTGATTTATGGTCTAATTTTCAGAGGGGCAAGAGTAGCAGTCTGTAAAGA 488
 UY 61 GCTTACTTTTAAAGCTATGTAATCAATTCAGTTCGTCGTCTTTAAATC 120
 |||||||
 DB 489 GCTTACTTTTAAAGCTATGTAATCAATTCAGTTCGTCGTCTTTAAATC 548
 UY 121 AATGCTTTAATTAAGCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
 |||||||
 DB 549 AATGCTTTAATTAAGCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 608
 UY 181 AATGCTTTAATTAAGCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 194
 |||||||
 DB 609 AATGCTTTAATTAAGCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 622

RESULT 3
 101156
LOCUS 101156 1469 bp ss-DNA Linear PAT 21-MAY-1993
DEFINITION Sequence 1 from Patient US 4762914.
ACCESSION 101156
VERSION 101156.1 GI:313921
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1469)
AUTHORS Auer, P.E., Webb, A.C., Gebhrer, L., Bharel, G.A., Rosenwasser, L.J.,
 Ricu, A., and Wolff, S.M.
TITLE Truncated protein of Interleukin-1
JOURNAL Patent: US 4762914-A 1 09-AUG-1988;
 119 Wilson Dr.; Framingham, MA
COMMENT on Jul 30, 1993 this sequence replaced q1:285480.
FEATURES
 source
 1..1469
 /organism "unknown"
BASE COUNT 408 a 354 c 326 g 481 t
ORIGIN

Query Match 82.2% Score 194; DB 6; Length 1469;
 Host Local Similarity 100.0%; Pred. No. 1.9e-86;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 TTTGATTTATGGTCTAATTTTCAGAGGGGCAAGAGTAGCAGTCTGTAAAGA 60
 |||||||
 DB 1268 TTTGATTTATGGTCTAATTTTCAGAGGGGCAAGAGTAGCAGTCTGTAAAGA 1427
 UY 61 GCTTACTTTTAAAGCTATGTAATCAATTCAGTTCGTCGTCTTTAAATC 120
 |||||||
 DB 1428 GCTTACTTTTAAAGCTATGTAATCAATTCAGTTCGTCGTCTTTAAATC 1487

QY 121 AACGCTTAATTAAGAGTAATATATAGCTAGATTATTAATGGAATATTAT 180
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Db 1388 AAGTCTTTAATTAAGAGTAATATATATAGCTAGATTATTAATGGAATATTAT 1447
QY 181 AATAGCAAAATAT 194
|||||
Db 1448 AATAGCAAAATAT 1461

RESULT 4
LOCUS HUM1L1 1496 bp mRNA linear PRI 11-JUN-1993
DEFINITION Human monocyte interleukin 1 (IL-1) mRNA, complete cds.
ACCESSION K02770
VERSION K02770.1 GI:186268
KEYWORDS Interleukin; interleukin 1.
SOURCE Human endotoxin-stimulated monocyte, cDNA to mRNA, clones PA-26,
pcd-415 and pcd-1218.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1496)
Auron, P.E., Webb, A.C., Rosenwasser, L.J., Mucci, S.F., Rich, A.,
Wolff, S.M. and Dinarello, C.A.
Nucleotide sequence of human monocyte interleukin 1 precursor cDNA
Proc. Natl. Acad. Sci. U.S.A. 81 (24), 7907-7911 (1984)
MEDLINE 6083965
JOURNAL 85088517
COMMENT A potential poly-A signal is found at position 1484-1489. Two
basic sequences that could be sites for protein processing, similar
to those observed for peptide hormones, are found at positions
708-716 and 723-728.

FEATURES
source
Location/Qualifiers
1..1496
/organism="Homo sapiens"
/db_xref="taxon:9606"
<..1496
/product="IL-1 mRNA"
87..896
/note="Interleukin 1 precursor polypeptide"
/codon_start=1
/protein_id="AAA36106.1"
/db_xref="GI:307043"
/translation="MAEVPKLAEMKAYSGNEHDLFFPADGPKOMKCSFQDLDCPL
DGGLRLSDHHSKGFROASVVAAMDRLKMLVPCPOTFOENLSTFFPIFEEDP
IFPDWDNKAIVHDAVRSKLTLDSDQSKSVMSGPELKLHLOGDMQGVFESM
SFVGGESNKKIPVALIKRKNLYLSVLDKDKPTLOLESVDPKPKKKKKREVEN
KLEINNKLEFFSAOPNNYISTSOAENMPVFLGTRGGQDIDFTMPGVSS"

BASE COUNT 416 a 361 c 328 g 391 t
ORIGIN 104 bp upstream of A1ul site.

Query Match 82.2%; Score 194; DB 9; Length 1496;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGATTCATGGTCTAATTTATTCAGAGGGGCAAGAGTAGCAGTCTGTAAAGA 60
|||||
Db 1269 TTTTGATTCATGGTCTAATTTATTCAGAGGGGCAAGAGTAGCAGTCTGTAAAGA 1328

QY 61 GCGTACTTTTAAATAGCTAGATCAATTCATTGGAGTGGTCTCTTTAAATC 120
|||||
Db 1329 GCGTACTTTTAAATAGCTAGATCAATTCATTGGAGTGGTCTCTTTAAATC 1388

QY 121 AAGTCTTTAATTAAGAGTAATATATAGCTAGATTATTAATGGAATATTAT 180
|||||
Db 1389 AAGTCTTTAATTAAGAGTAATATATAGCTAGATTATTAATGGAATATTAT 1448

QY 181 AATAGCAAAATAT 194
|||||
Db 1449 AATAGCAAAATAT 1462

RESULT 5

HUM1L1C
LOCUS HUM1L1C 1496 bp mRNA linear PRI 06-JAN-1995
DEFINITION Human monocyte interleukin mRNA, complete cds.
ACCESSION M54933.1 M38756
VERSION M54933.1 GI:186287
KEYWORDS Interleukin 1.
SOURCE Human monocyte, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1496)
Webb, A.C., Dinarello, C.A., Rosenwasser, L.J., Mucci, S.F., Rich, A.,
Wolff, S.M. and Auron, P.E.
Nucleotide sequence of human monocyte interleukin 1 precursor cDNA
Adv. Gene Technol. 22, 339-340 (1985)
JOURNAL
FEATURES
source
Location/Qualifiers
1..1496
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="2q12-q21"
/tissue_type="monocyte"
1..1496
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1..1496
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88..897
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/note="precursor protein"
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/product="interleukin 1"
/protein_id="AAA59136.1"
/db_xref="GI:186288"
/db_xref="SDB:G00-120-695"
/translation="MAEVPKLAEMKAYSGNEHDLFFPADGPKOMKCSFQDLDCPL
DGGLRLSDHHSKGFROASVVAAMDRLKMLVPCPOTFOENLSTFFPIFEEDP
IFPDWDNKAIVHDAVRSKLTLDSDQSKSVMSGPELKLHLOGDMQGVFESM
SFVGGESNKKIPVALIKRKNLYLSVLDKDKPTLOLESVDPKPKKKKKREVEN
KLEINNKLEFFSAOPNNYISTSOAENMPVFLGTRGGQDIDFTMPGVSS"

BASE COUNT 416 a 367 c 322 g 391 t
ORIGIN

Query Match 82.2%; Score 194; DB 9; Length 1496;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGATTCATGGTCTAATTTATTCAGAGGGGCAAGAGTAGCAGTCTGTAAAGA 60
|||||
Db 1269 TTTTGATTCATGGTCTAATTTATTCAGAGGGGCAAGAGTAGCAGTCTGTAAAGA 1328

QY 61 GCGTACTTTTAAATAGCTAGATCAATTCATTGGAGTGGTCTCTTTAAATC 120
|||||
Db 1329 GCGTACTTTTAAATAGCTAGATCAATTCATTGGAGTGGTCTCTTTAAATC 1388

QY 121 AAGTCTTTAATTAAGAGTAATATATAGCTAGATTATTAATGGAATATTAT 180
|||||
Db 1389 AAGTCTTTAATTAAGAGTAATATATAGCTAGATTATTAATGGAATATTAT 1448

QY 181 AATAGCAAAATAT 194
|||||
Db 1449 AATAGCAAAATAT 1462

RESULT 6
LOCUS E00846 1507 bp RNA linear PRI 29-SEP-1997
DEFINITION cDNA sequence for human IL-1.
ACCESSION E00846
VERSION E00846.1 GI:2169107
KEYWORDS JP 1986119191-A/1.
SOURCE unidentified.
ORGANISM unclassified.


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Db      8770  GCGTACGTTTAAAGCTATGAGATCAATTCATTGGACGTGCTGCTCTTTAAATC 8829
QY      121  AAGTCCCTTAATTAAGAGTGAATAATATAGCTCAGATTTATTAATGCAATTTAT 180
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Db      8830  AAGTCCCTTAATTAAGAGTGAATAATATAGCTCAGATTTATTAATGCAATTTAT 8889
QY      181  AATGAGCAAAATAT 194
          |||||||
Db      8890  AATGAGCAAAATAT 8903

RESULT 9
LOCUS    AX067266                      9721 bp    DNA        linear    PAT 24-JAN-2001
DEFINITION Sequence 2 from Patent WO0100880.
ACCESSION AX067266
VERSION  AX067266.1  GI:1254890
KEYWORDS
SOURCE   human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Moleleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
  1 (bases 1 to 9721)
  Duff, G.W., Cox, A., Camp, N.J. and di Giovine, F.S.
  Diagnostics and therapeutics for diseases associated with an 11-1
  inflammatory haplotype
  Patent: WO 0100880-A 2 04-JAN-2001;
  Interleukin Genetics, Inc. (US)
FEATURES
  source
    1..9721
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    /db_xref="taxon:9606"
BASE COUNT  2661 a 2328 c 2122 g 2608 t 2 others
ORIGIN
Query Match      82.2%; Score 194; DB 6; Length 9721;
Best local Similarity 100.0%; Pred. No. 1,2e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTGTGATTCATTCGCTAATTTATTCAGAGGGGCAAGAGTACGAGTGTCTGTAAAGA 60
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Db      8710  TTGTGATTCATTCGCTAATTTATTCAGAGGGGCAAGAGTACGAGTGTCTGTAAAGA 8769
QY      61  GCTTACTTTTAAAGTATGATGATCAATTTGAGTGTGTCTCTTTAAATC 120
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Db      8770  GCTTACTTTTAAAGTATGATGATCAATTTGAGTGTGTCTCTCTTTAAATC 8829
QY      121  AAGTCCCTTAATTAAGAGTGAATAATATAGCTCAGATTTATTAATGCAATTTAT 180
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Db      8830  AAGTCCCTTAATTAAGAGTGAATAATATAGCTCAGATTTATTAATGCAATTTAT 8889
QY      181  AATGAGCAAAATAT 194
          |||||||
Db      8890  AATGAGCAAAATAT 8903

RESULT 10
LOCUS    AX469435                      9721 bp    DNA        linear    PAT 16-JUL-2002
DEFINITION Sequence 1 from Patent WO0222877.
ACCESSION AX469435
VERSION  AX469435.1  GI:21901721
KEYWORDS
SOURCE   human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
  1
  Hill, J.A., Wang, Z.C., Anderson, D.J. and Yunis, E.J.
  Variants of 11-1 beta gene and cdk6 gene for diagnosing unexplained
  recurrent pregnancy loss
  Patent: WO 0222877-A 1 21-MAR-2002;
  THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) : LANA-FARRER CANCER

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INSTITUTE, INC. (US)
FEATURES
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    /organism="Homo sapiens"
    /db_xref="taxon:9606"
BASE COUNT  2661 a 2328 c 2122 g 2608 t 2 others
ORIGIN
Query Match      82.2%; Score 194; DB 6; Length 9721;
Best local Similarity 100.0%; Pred. No. 1,2e-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTGTGATTCATTCGCTAATTTATTCAGAGGGGCAAGAGTACGAGTGTCTGTAAAGA 60
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Db      8710  TTGTGATTCATTCGCTAATTTATTCAGAGGGGCAAGAGTACGAGTGTCTGTAAAGA 8769
QY      61  GCTTACTTTTAAAGTATGATGATCAATTTGAGTGTGTCTCTTTAAATC 120
          |||||||
Db      8770  GCTTACTTTTAAAGTATGATGATCAATTTGAGTGTGTCTCTCTTTAAATC 8829
QY      121  AAGTCCCTTAATTAAGAGTGAATAATATAGCTCAGATTTATTAATGCAATTTAT 180
          |||||||
Db      8830  AAGTCCCTTAATTAAGAGTGAATAATATAGCTCAGATTTATTAATGCAATTTAT 8889
QY      181  AATGAGCAAAATAT 194
          |||||||
Db      8890  AATGAGCAAAATAT 8903

RESULT 11
LOCUS    HST11B                      9721 bp    DNA        linear    PRI 26 JUN 1997
DEFINITION Human gene for prointerleukin 1 beta.
ACCESSION X04500
VERSION  X04500.1  GI:33788
KEYWORDS  Interleukin 1 beta.
SOURCE   Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
  1 (bases 1 to 9721)
  Clark, R.D., Collins, K.L., Gandy, M.S., Webb, A.C. and Auron, P.E.
  Genomic sequence for human prointerleukin 1 beta: possible
  evolution from a reverse transcribed prointerleukin 1 alpha gene
  Nucleic Acids Res. 14 (20): 7897-7914 (1986)
JOURNAL  87040762
MEDLINE  3490654
PubMed
COMMENT  Data kindly reviewed (13-MAY-1988) by Clark R.D.
FEATURES
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    /note="TATA-box like sequence"
    /note="1576..1581"
    /note="1809..1816"
    /note="1859..1866"
    /note="1903..1909"
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    /note="1"
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    /note="pol. viral enhancer core sequence"
    /note="2006..2465"
    /note="1"
    /note="2039..2055"
    /note="direct repeat 2"
    /note="2291..2297"
    /note="pol. viral enhancer core sequence"
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    misc_feature
  misc_feature
  intron
  repeat_region
  misc_feature

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                /protein_id="CA28185.1"
                /db_xref="GI:312408"
                /db_xref="SWISS-PROT:P01584"
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                LFFQWMEAVVHDAVPSNCTIROSQKSLVMSGYELKALHLDQDQEDQVFSM
                SPVQGESNRKIPVALGCKENLYLSTVLKDDKDTQLDSVDKRNPKKKEKPEVN
                KLENNKLEFSAPFDMVYSTSQAFNMFVADIKKGQDITLPEFMQVSS"
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                complement(2714..2721)
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misc_location 4274..4279
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                5327..5873
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exon 5874..6038
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                6039..7274
                /number=5
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Query Match 82.28; Score 194; Dh 9; Length 9721;
Host Local Similarity 100.0%; Pred. No. 1,20-86;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8710 TTTGATTCATTCGTCTAATTATTCAAGAGGCGAGAGAGTACAGCTGTTGTAAGA 8769
|||||
Qy 61 GCGTACTTTTAAAGCATAGCAATTAATTCATTTGACCTGAGGCTGTCTTTAAAT 120
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Db 8770 GCGTACTTTTAAAGCATAGCAATTAATTCATTTGACCTGAGGCTGTCTTTAAAT 8829
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Qy 121 AAGCTTTTAAATTAAGCTAATAATATATATATATATATTTAAATGGAATATAT 180
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Db 8830 AAGCTTTTAAATTAAGCTAATAATATATATATATATATTTAAATGGAATATAT 8889
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Qy 181 AATAGCAATAT 194
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Db 8896 AATAGCAATAT 8903
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RESULT 12
AX419978 1382 bp mRNA linear PAT 18-JUN-2002
LOCUS AX419978
DEFINITION Sequence 315 from patent WO0198537.
ACCESSION AX419978
VERSION AX419978.1 GI:21524445
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
  Lyanchikov V., Alawi H., Dong P., Netl R.P. and Venter J.J.
  Nucleic acid accessible hydration sites
  Patent: WO 0198537-A 315 27-DEC-2001;
  FILED WAVE TECHNOLOGIES, INC. (US)
FEATURES
  source
    1..1382
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
BASE COUNT 480 a 334 c 308 g 460 t
ORIGIN
Query Match 80.18; Score 189; Dh 6; Length 1382;
Host Local Similarity 100.0%; Pred. No. 5,20-84;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 ATTGATGCTCTATTATTATTCGAAGAGGAGAGACTAGTAGTGCTGTGTAAGCAAGCTA 65
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Db 1183 ATTGATGCTCTATTATTATTCGAAGAGGAGAGACTAGTAGTGCTGTGTAAGCAAGCTA 1242
|||||
Qy 66 GTTTTAAATAGCTATGCAATTCATTTGGAATGGGCTGCTGTGTAATCAAGCT 125
|||||
Db 1243 GTTTTAAATAGCTATGCAATTCATTTGGAATGGGCTGCTGTGTAATCAAGCT 1402
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Qy 126 GTTTTAAATAGCTAATAATATATATATATATATATATATATATATATATATATAT 185
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Db 1403 GTTTTAAATAGCTAATAATATATATATATATATATATATATATATATATATATAT 1462
|||||
Qy 186 ACCAATAT 194
|||||
Db 1363 ACCAATAT 1371
|||||
RESULT 13
HSPROT18 1473 bp mRNA linear PAT 06-DEC-1990
LOCUS HSPROT18
DEFINITION Human mRNA for proinfectin-1 beta.
ACCESSION X56087
VERSION X56087.1 GI:35662
KEYWORDS proinfectin 1; proinfectin 1 beta.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
  Kotenko S.V., Bulenkov M.T., Volko V.P., Epishin S.M.,

```

Lomakin, I.B., Emel'yanov, A.V., Kozlov, A.P., Korusova, V.G.,
Kotlov, A.Y., Kurbatova, T.V., Reshetnikov, V.L., Simbirskiy, A.S.,
Keflinskii, S.A. and Vinetskii, Y.P.
Cloning of the cDNA coding for human prointerleukin-1 alpha and
prointerleukin-1 beta
Dokl. Akad. Nauk SSSR 309 (4), 1005-1008 (1989)

JOURNAL MEDLINE

90249285

2635664

FEATURES

source

location/Qualifiers
1..1473

/organism="Homo sapiens"

/db_xref="taxon:9606"

/cell_type="monocyte"

/tissue_type="blood"

/dev_stage="adult"

58..867

/gene="proil-1 beta"

58..867

/gene="proil-1 beta"

/codon_start=1

/product="prointerleukin-1 beta"

/protein_id="CAA39567.1"

/db_xref="GI:35663"

/translation="MAVPELASEMAYVSGNEDLFFEDGSKMKCSFDDIDICPL
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58..864

/gene="proil-1 beta"

/product="prointerleukin-1 beta"

BASE COUNT 408 a 353 c 325 g 387 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 5.2e-84;

Matches 189: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

80.1%; Score 189; DB 9; Length 1473;

Query 6 ATTCATTCGCTTAATTATTCGAAGGGGGGCAAGACTAGCTGTCTGTAAGAAGCCCTA 65

1242 ATTCATTCGCTTAATTATTCGAAGGGGGGCAAGACTAGCTGTCTGTAAGAAGCCCTA 1301

66 GTTTTAATAGCTATGGAATCAATTCATTGAGCTGTCTCTTTAAATCAAGTC 125

1302 GTTTTAATAGCTATGGAATCAATTCATTGAGCTGTCTCTTTAAATCAAGTC 1361

126 CTTTAATTAAGCTGAAATATATTAAGCTGAGATTTTAATGAAGATTTTAAATG 185

1362 CTTTAATTAAGCTGAAATATATTAAGCTGAGATTTTAATGAAGATTTTAAATG 1421

186 AGCAAAATAT 194

1422 AGCAAAATAT 1430

RESULT 14

LOCUS AR030386 1497 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 10 from patent US 5861267.

ACCESSION AR030386

VERSION AR030386.1 GI:5943600

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1497)

AUTHORS Su, M.

TITLE Methods, nucleotide sequences and host cells for assaying exogenous

and endogenous protease activity

Patent: US 5861267-A 10 19-JAN-1999;

location/Qualifiers

1..1497

JOURNAL

FEATURES

source

1..1497

BASE COUNT 411 a 365 c 331 g 390 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 5.2e-84;

Matches 189: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

80.1%; Score 189; DB 6; Length 1497;

Query 6 ATTCATTCGCTTAATTATTCGAAGGGGGGCAAGACTAGCTGTCTGTAAGAAGCCCTA 65

1271 ATTCATTCGCTTAATTATTCGAAGGGGGGCAAGACTAGCTGTCTGTAAGAAGCCCTA 1330

66 GTTTTAATAGCTATGGAATCAATTCATTGAGCTGTCTCTTTAAATCAAGTC 125

1331 GTTTTAATAGCTATGGAATCAATTCATTGAGCTGTCTCTTTAAATCAAGTC 1390

126 CTTTAATTAAGCTGAAATATATTAAGCTGAGATTTTAATGAAGATTTTAAATG 185

1391 CTTTAATTAAGCTGAAATATATTAAGCTGAGATTTTAATGAAGATTTTAAATG 1450

/organism="unknown"

BASE COUNT 411 a 365 c 331 g 390 t

ORIGIN

Query Match

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Matches 189: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

80.1%; Score 189; DB 6; Length 1497;

Query 6 ATTCATTCGCTTAATTATTCGAAGGGGGGCAAGACTAGCTGTCTGTAAGAAGCCCTA 65

1271 ATTCATTCGCTTAATTATTCGAAGGGGGGCAAGACTAGCTGTCTGTAAGAAGCCCTA 1330

66 GTTTTAATAGCTATGGAATCAATTCATTGAGCTGTCTCTTTAAATCAAGTC 125

1331 GTTTTAATAGCTATGGAATCAATTCATTGAGCTGTCTCTTTAAATCAAGTC 1390

126 CTTTAATTAAGCTGAAATATATTAAGCTGAGATTTTAATGAAGATTTTAAATG 185

1391 CTTTAATTAAGCTGAAATATATTAAGCTGAGATTTTAATGAAGATTTTAAATG 1450

186 AGCAAAATAT 194

1451 AGCAAAATAT 1459

RESULT 15

LOCUS E06734 1497 bp RNA linear PAT 29-SEP-1997

DEFINITION DNA encoding IL-1 beta.

ACCESSION E06734

VERSION E06734.1 GI:2174916

KEYWORDS JP 1994041185-A/5.

SOURCE Unidentified.

ORGANISM synthetic construct.

artificial sequences.

REFERENCE 1 (bases 1 to 1497)

AUTHORS Hiroaki, M., Shoji, Y., and Mizushima, Y.

TITLE OHOSPHODILGONOCLEVIDIDE AND ITS USE

JOURNAL Patent: JP 1994041185-A 5 15-FEB-1994;

1..T T KENRYUSHO:KK

PN JP 1994041185-A/5

PD 15-FEB-1994

PE 16-JUL-1992 JP 1992213519

PT HIGAKI MEGUMI, SHOJI YOKO, MIZUSHIMA YUTAKA

PC C07H21/04,A61K31/70,A61K31/70,C12P19/14;

CC strandness: Double;

CC topology: linear;

CC key

FT mat_peptide 1..1497

FT /product="IL-1 beta"

FT location/Qualifiers

1..1497

/organism="synthetic construct"

/db_xref="taxon:32630"

BASE COUNT 411 a 365 c 331 g 390 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 5.2e-84;

Matches 189: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

80.1%; Score 189; DB 6; Length 1497;

Query 6 ATTCATTCGCTTAATTATTCGAAGGGGGGCAAGACTAGCTGTCTGTAAGAAGCCCTA 65

1271 ATTCATTCGCTTAATTATTCGAAGGGGGGCAAGACTAGCTGTCTGTAAGAAGCCCTA 1330

66 GTTTTAATAGCTATGGAATCAATTCATTGAGCTGTCTCTTTAAATCAAGTC 125

1331 GTTTTAATAGCTATGGAATCAATTCATTGAGCTGTCTCTTTAAATCAAGTC 1390

126 CTTTAATTAAGCTGAAATATATTAAGCTGAGATTTTAATGAAGATTTTAAATG 185

1391 CTTTAATTAAGCTGAAATATATTAAGCTGAGATTTTAATGAAGATTTTAAATG 1450

Tue Mar 18 16:20:48 2003

us-09-247-874c-2_copy_8710_8945.oli.rge

Page 8

QY 186 ACFAAATAT 194
|||||
DB 1451 ACFAAATAT 1459

Search completed: March 17, 2003, 21:05:14
Job Time : 1157 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1994 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 17, 2003, 17:37:19 ; Search time 224 Seconds
(without alignments)
2172.641 Million cell updates/sec

Title: US-09-247-874C-2_COPY_8710_8945

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SID22/qcqdada/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	236	100.0	9721	21	AAA50175 Human interleukin-
2	234.4	99.3	9721	20	AAK75924 Human interleukin-
3	234.4	99.3	9721	21	AAE20945 Human interleukin-
4	234.4	99.3	9721	21	AAE63768 Human IL-1B gene.
5	234.4	99.3	9721	21	AAA50174 Human interleukin-
6	234.4	99.3	9721	21	AAA34823 Human adenosine re
7	234.4	99.3	9721	22	AAAT27666 IL-1B DNA. Uniden
8	234.4	99.3	9721	22	AAC91434 Human IL-1B nucleo
9	234.4	99.3	9721	24	AAJ35192 Human prointerleuk

10	234.4	99.3	29433	21	AAE20950 Human interleukin-
11	234.4	99.3	29433	21	AAE34828 Human adenosine re
12	234.4	99.3	209273	21	AAE21437 Human factor-relat
13	231.8	98.2	7824	16	AAO74052 Human interleukin-
14	231.8	98.2	7824	22	AAH24368 Human IL-1B gene.
15	231.8	98.2	14690	20	AAH24368 Human IL-1B gene.
16	230.2	97.5	7824	24	ABK50291 Human interleukin
17	230.2	97.5	7824	24	ABK50293 Human interleukin
18	229.6	97.3	1507	6	AAH50060 Sequence encoding
19	229.6	97.3	1507	14	AAH50081 Human interleukin-
20	226.4	95.9	1404	7	AAH60283 Sequence encoding
21	226.4	95.9	1404	8	AAH70505 Sequence encoding
22	226.4	95.9	1404	14	AAO51110 Human interleukin-
23	226.2	95.8	1497	21	AAE20944 Human interleukin-
24	226.2	95.8	1497	21	AAH44822 Human adenosine re
25	226.2	95.8	1497	24	ABK81933 Human cDNA differe
26	224.8	95.3	656	21	AAH51659 Interleukin 1-beta
27	224.8	95.3	1496	21	AAE20946 Human interleukin-
28	224.8	95.3	1496	21	AAH34824 Human adenosine re
29	224.6	95.2	1497	15	AAO58462 IL-1 beta gene.
30	205.8	87.2	1514	21	AAE25973 cDNA encoding huma
31	200.8	85.1	1382	24	AAH46348 Human gene signatu
32	195	82.6	454	16	AAT20507 Human IL-1ra RAG c
33	170	72.0	8639	20	AAH02995 Monkey IL-2 beta g
34	163	69.1	1458	11	AAO05593 Sequence encoding
35	119.6	50.7	1429	13	AAO22825 Forcine pro-interl
36	91	38.6	8760	15	AAO74473 Bayline interleukin
37	70.6	29.9	1750	9	AAH80433 Rat IL-1beta gene.
38	69.2	29.3	1322	10	AAH90514 Rat sequence diffi
39	69.2	29.3	1327	14	AAO49458 Mouse spliced tran
40	67.4	28.6	1329	24	ABK63523 Human interleukin-
41	60	25.4	1330	14	AAO40567 Mouse interleukin-
42	58.4	24.7	60	24	AAH38537 Probe used to dete
43	58.4	24.7	1339	21	AAH94191 Probe used to dete
44	44	18.6	44	21	AAH50182
45	44	18.6	44	21	AAH50184

ALIGNMENTS

RESULT 1	AAA50175	standard: ONA: 9721 BP.
ID	AAA50175	
AC	AAA50175:	
DT	07-NOV-2000	(first entry)
XX	Human interleukin-1 beta allele 2 (+6912).	
XX	Interleukin-1 beta; IL-1B; human; polymorphism; inflammation;	
XX	coronary artery disease; osteoporosis; nephropathy;	
XX	alopecia areata; Graves disease; systemic lupus erythematosus;	
XX	lichen sclerosis; ulcerative colitis; diabetic retinopathy;	
XX	periodontal disease; juvenile chronic arthritis; psoriasis;	
XX	insulin dependent diabetes; asthma; lung fibrosis;	
XX	chronic inflammatory liver disease; rheumatoid arthritis;	
XX	chronic inflammatory lung disease; antiinflammatory; osteoporotic;	
XX	dermatological; immunosuppressive; antidiabetic; antithyroid;	
XX	antiarthritic; antineumatic; antitachycardic; antipsoriatic;	
XX	hepatotropic; antitumor; diagnosis; therapy; ds.	
XX	Homo sapiens.	
XX	key	Location/Qualifiers
XX	variation	replace(8904,c)
XX	FT	/tag a
XX	FT	/note- "IL-1B allele 2 (+6912)"
XX	PN	W0200047619-A1.
XX	PD	17-NOV-2000.

RESULT 3
AAE20945
ID AAF20945 standard; DNA: 9721 BP.
XX
AC AAF20945:
XX
DT 14-MAR-2001 (first entry)
XX
DE Human Interleukin-1 polynucleotide fragment #2512.
XX
KW low adenovine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytosolic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN W0200062736-A2.
XX
PD 26-OCT-2000.
XX
PP 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 990S-0127958.
XX
PA (UPEC-) UNIV EAST CAROLINA.
XX
PA (NYCE/) NYCE J W.
XX
PI Nyce JW:
XX
DR WPI: 2000-679539/66.
XX
PT Low adenovine (A) content antisense oligonucleotides which do not
PT trigger adenovine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure: Page 230-232; 1592pp; English.
XX
XX The present invention describes low adenovine (A) content antisense
XX oligonucleotides and compositions (I) comprising them. In the antisense
XX oligonucleotides the A is replaced by a 'Universal' or alternative base.
XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
XX immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
XX The antisense oligonucleotides and (I) can be used to down-regulate the
XX expression and/or activity of target polypeptides associated with
XX lung/respiratory disorders and malignancies, such as stimulating and
XX activating peptide factors and transmitters, transcription factors,
XX immunoglobulins and antibodies, antibody receptors, cytokines and
XX chemokines, endogenously produced specific and non-specific enzymes,
XX binding proteins, adhesion molecules and their receptors, cytokine and
XX chemokine receptors, adenovine receptors, bradykinin receptors, central
XX nervous system (CNS) and peripheral nervous and non-nervous system
XX receptors, CNS and peripheral nervous and non-nervous system peptide
XX transmitters, defensins, growth factors, vasoactive peptides and
XX receptors, binding proteins and malignancy associated proteins. The
XX antisense oligonucleotides may be used in this way to treat disorders
XX including respiratory obstruction (especially pulmonary obstruction
XX and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
XX and/or surfactant hypoproduction which are associated with a disease or
XX condition selected from pulmonary vasoconstriction, inflammation,
XX allergies, asthma, impeded respiration, respiratory distress syndrome
XX (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
XX hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
XX pulmonary transplantation rejection, pulmonary infections, bronchitis,
XX and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
XX fragments and antisense oligonucleotides used in the exemplification of
XX the present invention.

XX
SQ Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other:
XX
Query Match 99.3%; Score 234.4; DI 21; Length 9721;
Best Local Similarity 99.6%; Pred. No. 2,6e-45;
Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TTTTGATGATGGTCTATTATTCAGAGGGGCAAGAGTAGTGCTGTAAAGA 60
DB 8710 TTTTGATTCATGTTGCTATTATTCAGAGGGGCAAGAGTAGTGCTGTAAAGA 8769
QY 61 GCCATGTTTAAATGCTATGATGAAATCAATTCATTTGCACTGCTGCTTTAAATC 120
DB 8770 GCGTATTTTAAATGCTATGAAATCAATTCATTTGCACTGCTGCTTTAAATC 8829
QY 121 AAGTCCTTTAAATTAAGACTGAAATATATACCTGACATTAATTAAGCAATATTAAT 180
DB 8830 AAGTCCTTTAAATTAAGACTGAAATATATACCTGACATTAATTAAGCAATATTAAT 8889
QY 181 AAGTACGCAATATGATGCTGCAATGCTGCTGCAATATGCTGCAATGCAATGCAAT 236
DB 8890 AAGTACGCAATATGATGCTGCAATGCTGCTGCAATATGCTGCAATGCAATGCAAT 8945
RESULT 4
AAE63768
ID AAF63768 standard; DNA: 9721 BP.
XX
AC AAF63768;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human IL-1b gene.
XX
KW Human; IL-1b; interleukin-1b; cytostatic; antiinflammatory;
KW immunosuppressive; dermatological; antimicrobial; antiarthritic;
KW IL-1 receptor antagonist; tumor necrosis factor alpha antagonist
KW interstitial lung disease; interstitial pneumonia; pulmonary fibrosis;
KW rheumatoid arthritis; systemic lupus erythematosus; Sjogren's syndrome;
KW systemic sclerosis; dermatomyositis; chromosome 2; ds.
XX
OS Homo sapiens.
XX
PN W0200060117-A2.
XX
PD 12-OCT-2000.
XX
PP 11-MAR-2000; 2000WO-US08492.
XX
PR 02-APR-1999; 990S-0286108.
XX
PA (INTE-) INTERLEUKIN GENETICS INC.
XX
PA Duff GW, Di Giovine FS, Whyte M:
XX
DR WPI: 2000-656234/63.
XX
PT Method for predicting the risk of interstitial lung disease, comprising
PT detecting an interleukin-1 receptor antagonist allele and tumor
PT necrosis alpha allele or an allele in linkage disequilibrium with
PT either of these alleles -
XX
XX Claim 6; Fig 2; 102pp; English.
XX
XX The present sequence is provided in a specification relating to a method
XX for determining whether a subject has or is predisposed to develop an
XX interstitial lung disease. The method involves detecting an interleukin-1
XX receptor antagonist (IL-1RN) (-2018) allele 2, a tumor necrosis alpha
XX (TNF-A) (-308) allele 2, or an allele in linkage disequilibrium with
XX either of these two alleles. The method may be used to determine whether
XX a subject has or is predisposed to develop an interstitial pneumonia or a
XX pulmonary fibrosis and other disorders such as rheumatoid arthritis,
XX systemic lupus erythematosus, Sjogren's syndrome, systemic sclerosis.


```

XX FN WO200009525-A2.
XX ED 24-FEB-2000.
XX XX
XX FP 03-AUG-1999; 99WO-US17712.
XX XX
XX PR 03-AUG-1998; 98US-0095212.
XX XX
XX PA (OIEC-) UNIV EAST CAROLINA.
XX XX
XX NYce JW;
XX XX
XX WP: 2000-205971/18.
XX XX
XX PS Disclosure: Page 673-675; 1343pp; English.
XX XX
XX CC The present invention describes a new composition comprising an
XX CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
XX CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
XX CC inflammation. The ON can have antiinflammatory, antiallergic,
XX CC antiasthmatic, cytostatic and analgesic activities. The compositions are
XX CC useful for the treatment of diseases associated with inflammation,
XX CC impaired airways, including lung disease and diseases whose secondary
XX CC effects affect the lungs of a subject. They can be used for treating
XX CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies,
XX CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
XX CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
XX CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
XX CC carcinomas, and cancers which may metastasize to the lungs, including
XX CC breast and prostate cancer. The reduction of the adenosine content of
XX CC the ONs reduces side effects. The A-containing ONs break down with the
XX CC release of deoxyadenosine which activates adenosine receptors causing the
XX CC bronchoconstriction and inflammation. AAA3213 to AAA5312 represent the
XX CC nucleotide sequences given in the sequence listing from the present
XX CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
XX CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
XX CC differ from the previously named sequences. SEQ ID NO:11 to 1680
XX CC (AAA3223 to AAA3992) are specifically claimed ONs from the present
XX CC invention. N.B. Sequences given in the disclosure of the present
XX CC invention do not match up with their corresponding SEQ ID NO: sequences
XX CC given in the sequence listing.
XX XX
XX SO Sequence 9721 BP: 2661 A; 2328 C; 2122 G; 2608 T; 2 other:

Query Match          99.3%; Score 234.4; DB 21; Length 9721;
Best Local Similarity 99.6%; Pred. No. 2,6e-45;
Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

01 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
02 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
03 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
04 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
05 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
06 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
07 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
08 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
09 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
10 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
11 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
12 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
13 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
14 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
15 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
16 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
17 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
18 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
19 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
20 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
21 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
22 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
23 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
24 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
25 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
26 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
27 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
28 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
29 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
30 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
31 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
32 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
33 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
34 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
35 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
36 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
37 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
38 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
39 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
40 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
41 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
42 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
43 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
44 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
45 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
46 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
47 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
48 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
49 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
50 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
51 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
52 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
53 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
54 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
55 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
56 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
57 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
58 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
59 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
60 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
61 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
62 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
63 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
64 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
65 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
66 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
67 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
68 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
69 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
70 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
71 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
72 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
73 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
74 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
75 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
76 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
77 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
78 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
79 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
80 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
81 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
82 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
83 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
84 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
85 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
86 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
87 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
88 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
89 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
90 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
91 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
92 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
93 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
94 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
95 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
96 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
97 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
98 TTTTATTCATTGGCTCAATTATTTCAAAGGCGGACAGACGACGCTCTGTATAAGA 60
99 TTTTATTCATTGGCT
```

XX	AAZ27666;
AC	
XX	02-APR-2001 (first entry)
DT	
XX	
DE	IL-1B DNA.
XX	
XX	IL-1; interleukin; inflammation; infection; ds
OS	Unidentified.
XX	
PV	W0200100880-AZ.
XX	
PD	04-JAN-2001.
XX	
XX	30-JUN-2000; 2000MO-US18318.
FE	
XX	30-JUN-1999; 99US-0345217.
PR	
XX	(INTE-) INTERLEUKIN GENETICS INC.
PA	
PI	Duff GW, Cox A, Camp NJ, Di Giovine FS;
XX	WPJ: 2001-102903/11.
DR	
XX	
PT	Determining whether a subject has or is predisposed to disease
XX	associated with IL-1 polymorphism involves determining presence of
PI	marker or allele comprising IL-1 inflammatory haplotype -
XX	
PS	Disclosure: Fig 4; 84pp; English.
XX	
CC	The present invention relates to a new method for determining whether
CC	a subject has or is predisposed to developing a disease or condition
CC	that is associated with an IL (interleukin)-1 inflammatory haplotype,
CC	comprises detecting at least one allele of the haplotype where the
CC	presence of the allele indicates that the subject is predisposed to
CC	the development or has the disease or condition.
CC	The method is useful for determining whether a subject has or is
CC	predisposed to inflammatory disease, a degenerative disease, an
CC	immunological disorder, an infectious disease, trauma induced disease,
CC	or cancer. The above conditions associated with an IL-1 inflammatory
CC	haplotype can be treated or prevented by administering a therapeutic
CC	that compensates for a causative mutation that is in linkage
CC	disequilibrium with at least one IL-1 polymorphism.
XX	
SQ	Sequence 9721 BP: 2661 A; 2328 C; 2122 G; 2607 T; 3 other:
	Query Match 99.3%; Score 234.4; DH 22; Length 9721;
	Best Local Similarity 99.6%; Pred. No. 2,60-45;
	Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
OY	1 TTGTATTCATTGTTGGTAAATTTATTCGAAGGCGGCAGCAAGTAGCAGTGCTCTGTAAGA 60
DB	8710 TTTGATTTATTCGCTATTTATTCGAAGGCGGCAGCAGTAGCAGTCTCTGTAAGAAA 8769
OY	61 GCCTAGTTTTATACCTATGCAATCAATTGCACTGGTGCTCTCTTAAATC 120
DB	8770 GGCTAGTTTTATATACCTATGCAATCAATTGCACTGGTGCTCTCTTAAATC 8829
OY	121 AAGTCCTTAATTAAGACTGAATAATATATAGCTCAGATTATTTAATGGAATATTA 180
DB	8830 AAGTCCTTAATTAAGACTGAATAATATATAGCTCAGATTATTTAATGGAATATTA 8889
OY	181 AAATGAGCAATATATATACTGTCCAATGTTTCGAAATTAACCTTCAGTAACAANA 236
DB	8890 AAATGAGCAATATATATACTGTCCAATGTTTCGAAATTAACCTTCAGTAACAANA 8945
	RESULT 8
ID	AAC91434
XX	AAC91434 standard; DNA: 9721 BP.
AC	AAC91434;

```

XX
XX 20 MAR 2001 (first entry)
XX
XX Human IL-1b nucleotide sequence.
XX
XX Human IL-1A; interleukin-1alpha; IL-1b; interleukin-1beta; IL-1RN;
XX interleukin-1 receptor antagonist; vasotrophic; antiinflammatory;
XX hypotensive; anticonvulsant; antilipemic; arterial restenosis;
XX restenosis associated allele; RAA; occlusive cardiovascular disorder;
XX restenosis detection; ds.
XX
XX Homo sapiens.
XX
XX W0200071754 A2.
XX
XX 40 NOV-2000.
XX
XX 24 MAY-2000; 2000W0-0514299.
XX
XX 24-MAY-1999; 9905 0317674.
XX 01-NOV-1999; 9905-0431352.
XX
XX (UNTE.) INTERLEUKIN GENETICS INC.
XX
XX Kottman KS, Duff GW, Crossman MC, Francis SE, Stephenson K;
XX WP1; 2001-025173/03.
XX
XX PT Diagnosing or determining susceptibility to developing restenosis
XX PT involves detecting restenosis associated allele in a nucleic acid
XX sample.
XX
XX PS Disclosure: Fig 2; 12pp; English.
XX
XX CC The present sequence is given in a specification relating to a method for
XX CC determining whether a subject has or is predisposed to developing an
XX CC arterial restenosis. The method comprises detecting a restenosis
XX CC associated allele (RAA) in a nucleic acid sample from the subject, where
XX CC detection of the RAA indicates that the subject has or is predisposed to
XX CC the development of a restenosis. The restenosis associated allele
XX CC pattern permits the diagnosis of occlusive cardiovascular disorder. The
XX CC diagnosis allows the most suitable treatment methods for restenosis to be
XX CC used, e.g., selecting therapies for initial vascular stenosis most likely
XX CC to avoid subsequent stenosis. The detection methods identify restenosis
XX CC therapeutics, agonists and antagonists, (proteins, peptides,
XX CC peptidomimetics, small molecules or nucleic acids, e.g., anti-sense,
XX CC ribozyme and triplex nucleic acids) which are used to treat restenosis.
XX
XX Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;
XX
XX Query Match 99.38; Score 234.4; DB 22; Length 9721;
XX Host Local Similarity 99.68; Prod. No. 2.6e-45;
XX Matches 245; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 TTTGATTGATTCGCTTAATTATTCGAGGAGTAAAGTACAGTGTCTGTAAAGA 60
XX DB 8710 TTTGATTGATTCGCTTAATTATTCGAGGAGTAAAGTACAGTGTCTGTAAAGA 8769
XX
XX QY 61 GCTTACTTTTAATGATTCGATTCATTCATTCGCTGCTGCTTTAAATC 120
XX DB 8770 GCTTACTTTTAATGATTCGATTCATTCATTCGCTGCTGCTTTAAATC 8829
XX
XX QY 121 AATTCCTTTAATTAAGTATGAAATATATTAAGCTGATTTAAAGGATATTTAT 180
XX DB 8840 AATTCCTTTAATTAAGTATGAAATATATTAAGCTGATTTAAAGGATATTTAT 8889
XX
XX QY 181 AATTCAGCAAAATATGACATGTTCAATGCTCGAATTAATTCAGTCAAGAAAA 236
XX DB 8890 AATTCAGCAAAATATGACATGTTCAATGCTCGAATTAATTCAGTCAAGAAAA 8945
XX
XX RESULT 9
XX AA035192

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XX
XX AA035192 standard; DNA; 9721 BP.
XX
XX AC AA035192;
XX
XX 25-JUL-2002 (first entry)
XX
XX DE Human prointerleukin-1 beta (IL-1 beta) gene.
XX
XX DE Unexplained recurrent pregnancy loss; immunologic reproductive failure;
XX URPL; prointerleukin-1beta; IL-1beta; human; ds.
XX
XX OS Homo sapiens.
XX
XX PN W0200222877-A2.
XX
XX 21-MAR-2002.
XX
XX 12-SEP-2001; 2001W0-0528465.
XX
XX 12-SEP-2000; 2000W0-241785p.
XX
XX (BCHM.) BRIGHAM & WOMEN'S HOSPITAL, INC.
XX (DAND.) DANA-FARBER CANCER INST. INC.
XX
XX H111 JA, Wang MC, Anderson MJ, Yunis EJ;
XX WP1; 2002-362362/49.
XX
XX PT Evaluating risk of unexplained recurrent pregnancy loss in a subject,
XX PT by testing presence of a variant in interleukin-1 beta promoter region
XX PT and/or in CpG6 gene Intron 1 region in a sample obtained from the
XX PT subject.
XX
XX PS Example 2 and 3; Page 51-54; 57pp; English.
XX
XX CC The invention relates to a method for evaluating and treating risk of
XX CC unexplained recurrent pregnancy loss (URPL) in a subject suspected of
XX CC having immunologic reproductive failure. The method involves testing a
XX CC sample obtained from the subject for the presence of a variant in the
XX CC human interleukin-1beta (IL-1beta) promoter region, and/or a variant
XX CC in the CpG6 gene Intron 1 region, where the presence of the variant
XX CC indicates an elevated risk of developing recurrent pregnancy loss.
XX CC The present sequence is human prointerleukin-1 beta (IL-1 beta) gene.
XX
XX Sequence 9721 BP; 2661 A; 2328 C; 2122 G; 2608 T; 2 other;
XX
XX Query Match 99.38; Score 234.4; DB 24; Length 9721;
XX Host Local Similarity 99.68; Prod. No. 2.6e-45;
XX Matches 245; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 TTTGATTGATTCGCTTAATTATTCGAGGAGTAAAGTACAGTGTCTGTAAAGA 60
XX DB 8710 TTTGATTGATTCGCTTAATTATTCGAGGAGTAAAGTACAGTGTCTGTAAAGA 8769
XX
XX QY 61 GCTTACTTTTAATGATTCGATTCATTCATTCGCTGCTGCTTTAAATC 120
XX DB 8770 GCTTACTTTTAATGATTCGATTCATTCATTCGCTGCTGCTTTAAATC 8829
XX
XX QY 121 AATTCCTTTAATTAAGTATGAAATATATTAAGCTGATTTAAAGGATATTTAT 180
XX DB 8830 AATTCCTTTAATTAAGTATGAAATATATTAAGCTGATTTAAAGGATATTTAT 8889
XX
XX QY 181 AATTCAGCAAAATATGACATGTTCAATGCTCGAATTAATTCAGTCAAGAAAA 236
XX DB 8890 AATTCAGCAAAATATGACATGTTCAATGCTCGAATTAATTCAGTCAAGAAAA 8945
XX
XX RESULT 10
XX AA035192 standard; DNA; 29433 BP.
XX
XX AC AA035192;
XX
XX

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DT 14-MAR-2001 (first entry)
 XX DE Human interleukin-1 polynucleotide fragment #2517.
 XX
 XX Low adenosine antisense oligonucleotide: phosphorothioate; allergy;
 KM human; airway disorder; bronchoconstriction; lung inflammation;
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KM immunosuppressive; antiallergic; analgesic; hypotensive; cytosolic;
 KM respiratory obstruction; pulmonary obstruction; impeded respiration;
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 XX cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200062746-A2.
 XX
 PD 26-OCT-2000.
 XX
 XX 24-MAR-2000; 2000WO-US08020.
 XX
 XX 06-APR-1999; 990S-0127958.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (UYEC/) NYCE J W.
 XX
 XX NYCE JW:
 XX
 XX MPI: 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions.
 XX
 PS Disclosure: Page 221-227; 1592pp; English.
 XX
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (1) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (1) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiallergic, hypotensive and cytosolic activities.
 CC The antisense oligonucleotides and (1) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergies (e.g.
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAT18434 to AAT21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 XX
 SO Sequence 29433 BP; 8714 A; 6519 C; 5920 G; 8278 T; 2 other.
 Query Match 99.38; Score 234.4; DB 21; Length 29433;
 Best Local Similarity 99.68; Pred. No. 3e-45;
 Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTGATTCATTCGCTAAATTATTCGAAGGGGCGCAAGTAGAGTCTGTAAATA 60
 DB 22177 TTTTCATTCATTCGCTAAATTATTCGAAGGGGCGCAAGTAGAGTCTGTAAATA 22246
 QY 61 GCGTACTTTTAAATACCTATGGAATCAATTCATTTGAGTCTGCTCTTTAAATC 120
 DB 22237 GCGTACTTTTAAATACCTATGGAATCAATTCATTTGAGTCTGCTCTTTAAATC 22246
 QY 121 AAGTCTTTTAAATACCTATGGAATCAATTCATTTGAGTCTGCTCTTTAAATC 180
 DB 22297 AAGTCTTTTAAATACCTATGGAATCAATTCATTTGAGTCTGCTCTTTAAATC 22356
 QY 181 AAGTCTTTTAAATACCTATGGAATCAATTCATTTGAGTCTGCTCTTTAAATC 236
 DB 22357 AAGTCTTTTAAATACCTATGGAATCAATTCATTTGAGTCTGCTCTTTAAATC 22412
 RESULT 11
 AAA34828
 ID AAA34828 standard; DNA; 29433 BP.
 XX
 AC AAA34828;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 XX Human adenosine receptor related polynucleotide SEQ ID NO:2517.
 XX
 XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KM phosphorothioate; impeded respiration; inflammation; allergy;
 KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KM antiallergic; antiallergic; cytosolic; analgesic; impaired airway;
 KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KM cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 XX 03-AUG-1999; 99WO-US17712.
 XX
 XX 03-AUG-1999; 980S-0095212.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 XX NYCE JW:
 XX
 XX MPI: 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischaemia or
 PT cancers.
 XX
 PS Disclosure: Page 677-684; 1343pp; English.
 XX
 XX The present invention describes a new composition comprising an
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiallergic, cytosolic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including


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XX XX Key Location/Qualifiers
FH misc_difference 1331
FT /tag- a
FT /note- "N is undefined"
XX XX JP07123984-A.
XX XX 16-MAY-1995.
XX XX 05-NOV-1993; 93JP-0275852.
XX XX 05-NOV-1993; 93JP-0275852.
XX XX 05-NOV-1993; 93JP-0275852.
XX XX (HITB ) HITACHI CHEM CO LTD.
XX XX WPI: 1995-211627/28.
XX XX A primer for the detection and the determ. of a specific messenger
XX XX RNA - can detect and determine specific mRNA(s) with high
XX XX reliability
XX XX Example 18; page 17-20; 35pp; Japanese.
XX XX AA074052 is interleukin-1-beta cDNA and AA074019-21 are primers used for
XX XX the amplification of this cDNA. They are used specifically for the
XX XX detection and isolation of this sequence. The primers have the
XX XX advantage of high sensitivity and reliability and are useful in the
XX XX pharmaceutical industry.
SQ Sequence 7824 BP; 2099 A; 1905 C; 1624 G; 2195 T; 1 other:
Query Match 98.28; Score 231.8; DB 16; Length 7824;
Best Local Similarity 99.18; Pred. No. 1e-44;
Matches 233; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TTGGATTCATGCTCAATTATTCGAAGGGGCAAGAGTACGCTGCTGAAGAAG 61
DB 7153 TTTTATTCATGCTCAATTATTCGAAGGGGCAAGAGTACGCTGCTGAAGAAG 7212
QY 62 CCTAGTTTAAATAGCTATGCAATTCATTTGACCTGCTGCTCTTTAAATCA 121
DB 7213 CCTAGTTTAAATAGCTATGCAATTCATTTGACCTGCTGCTCTTTAAATCA 7272
QY 122 AGTCCTTTAATAGAGTGAATATATAGCTACATATTTAAATGGCAATATTATA 181
DB 7273 AGTCCTTTAATAGAGTGAATATATAGCTACATATTTAAATGGCAATATTATA 7332
QY 182 AATGACCAATATGATAGCTGCTCAATGCTGCTGAATAAAGTCTGCTGAAGAAA 236
DB 7333 AATGACCAATATGATAGCTGCTCAATGCTGCTGAATAAAGTCTGCTGAAGAAA 7387

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FT variation replace(346,T)
FT /tag- b
FT /standard_name- "Single nucleotide polymorphism"
FT 924...970
FT /tag- c
FT /number= 2
FT 1536...1587
FT /tag- d
FT /number= 3
FT 3576...3777
FT /tag- e
FT /number= 4
FT replace(4258,A)
FT /tag- f
FT /standard_name- "Single nucleotide polymorphism"
FT replace(4336,T)
FT /tag- g
FT /standard_name- "Single nucleotide polymorphism"
FT 4323...4487
FT /tag= h
FT /number= 5
FT 5723...5853
FT /tag- i
FT /number= 6
FT replace(6421,G)
FT /tag- j
FT /standard_name- "Single nucleotide polymorphism"
FT 6570...6782
FT /tag- k
FT /number= 7
FT replace(6883,A)
FT /tag- l
FT /standard_name- "Single nucleotide polymorphism"
FT W0200121639-A1.
FT 29-MAR-2001.
FT 20-SEP-2000; 2000WO-US25794.
FT 22-SEP-1999; 99US-0155412.
FT (GENA-) GENAISSANCE PHARM INC.
FT Chew A, Choi J, Denton RR, Nandabalan K, Stephens JC;
FT WPI: 2001-389617/41.
FT New polynucleotide useful for therapeutic purposes, comprises
FT nucleotide polymorphisms of Interleukin-1b gene
FT Claim 1; Fig 1; 57pp; English.
XX The present invention relates to an isolated polynucleotide comprising
XX a nucleotide sequence which is a polymorphic variant of the fully
XX defined 7821 base pair Interleukin-1 beta (IL1B) gene reference
XX sequence given in the specification or its fragment or complement.
XX CC The IL1B gene polymorphic variant is useful for therapeutic purposes,
XX CC for studying the expression and biological function of IL1B, for
XX CC developing drugs targeting this protein, and in diagnostics and
XX CC forensic applications. The method is useful for developing tests and
XX CC therapeutic treatments for inflammatory and immune disorders. The
XX CC present sequence is the 7821 bp IL1B gene reference sequence.
SQ Sequence 7824 BP; 2099 A; 1905 C; 1624 G; 2195 T; 1 other:
Query Match 98.28; Score 231.8; DB 22; Length 7824;
Best Local Similarity 99.18; Pred. No. 1e-44;
Matches 233; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TTGGATTCATGCTCAATTATTCGAAGGGGCAAGAGTACGCTGCTGAAGAAG 61
DB 7153 TTTTATTCATGCTCAATTATTCGAAGGGGCAAGAGTACGCTGCTGAAGAAG 7212

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2003, 17:38:45 : Search time 1149 Seconds

(without alignments)
5977.600 Million cell updates/sec

Title: US-09-247-874c-2_COPY_8710_8945

Perfect score: 236
Sequence: 1 ttltgacatcagcgaat.....ataacttactgaagaaa 236

Scoring table:
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

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1:  qb_da:*
2:  qb_hq:*
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8:  qb_pl:*
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11: qb_sls:*
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41: em_hq_vrt:*

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pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	234.4	99.3	614	11	G10509
2	234.4	99.3	9721	6	AX052806
3	234.4	99.3	9721	6	AX067266
4	234.4	99.3	9721	6	AX469435
5	234.4	99.3	9721	6	AX469435
6	231.8	98.2	7824	9	H00111B
7	231.8	98.2	17447	9	AT137079
8	231.8	98.2	154214	9	AC079753
9	230.2	97.5	1473	9	HSPRO11B
10	230.2	97.5	1522	9	BC008678
11	229.6	97.3	1507	6	E00846
12	229.6	97.3	1507	6	107942
13	226.4	95.9	1404	6	A21148
14	226.4	95.9	1404	6	F01230
15	226.4	95.9	1404	6	F11934
16	226.4	95.9	1404	6	E12090
17	226.4	95.9	1404	6	100228
18	226.2	95.8	1497	6	AR030386
19	226.2	95.8	1497	6	F06734
20	226.2	95.8	1497	9	H00111B
21	224.8	95.3	1496	6	AX027920
22	224.8	95.3	1496	6	H00111
23	224.8	95.3	1496	9	H00111C
24	205.8	87.2	1514	6	AR086559
25	205.8	87.2	1514	6	100729
26	200.8	85.1	1382	6	AX419478
27	200.4	84.9	1469	6	101156
28	163	69.1	1458	6	F02498
29	136.6	57.9	1476	4	FE320322
30	122.4	51.9	1473	4	EC092481
31	119.6	50.7	1429	6	A19155
32	91	38.6	8760	4	SSPIN1H
33	89.6	38.0	1458	4	P1611KN1H
34	76	32.2	1437	10	AE119622
35	70.6	29.9	1736	4	HOV11B
36	70.6	29.9	1736	4	103510
37	69.2	29.3	1327	6	F01884
38	69.2	29.3	1327	6	F05490
39	67.4	28.6	1329	6	AX401754
40	67.4	28.6	1329	10	RAT111B
41	62.6	26.5	1403	4	RAT1182
42	60	25.4	1340	6	E04743
43	58.4	24.7	1339	6	E55193
44	58.4	24.7	1339	10	M05111B
45	57	24.2	175022	2	AC103019

ALIGNMENTS

RESULT 1
LOCUS G10509
DEFINITION human STS CHUC.UTR.00699_X04500.P37183 clone UTR.00699_X04500,
sequence tagged site.
ACCESSION G10509.1 G1:942358
VERSION G10509.1
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens vector/pUCP1 host-E.coli dut+und+ (CH105) Marker
Selected genomic DNA prepared from XI individual of French
nationality.
ORGANISM Homo sapiens
Fukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 614)

AUTHORS Murray, J., Sheffield, V., Weber, J.L., Day, G., and Burtow, K.H.
TITLE Cooperative Human Linkage Center
JOURNAL Unpublished (1995)
COMMENT Synonyms: UTR_00699_X04500, CHC-UTR_00699_X04500.T36097
 Contact: Dr. Jeffrey C. Murray

URL The University of Iowa
 Department of Pediatrics, Iowa City, IA 52242, USA
 Tel: (319) 356-3508
 Fax: (319) 356-3347
 Email: jett-murray@uiowa.edu

Primer A: AGTACCTCTCTCTTTCAGG
Primer B: GTGAGGCTTTTAAATAAT
STS Size: 229
PCR Profile:

denature: 30 seconds at 94 degrees C
 annealing: 75 seconds at 55 degrees C
 extension: 15 seconds at 72 degrees C
 PCR cycles: 27
 extension: 6 minutes at 72 degrees C
Protocol:
 Template: 30ng genomic DNA
 Primers: each 1.5 pmole
 dNTPs: each 200 uM
 Taq Polymerase: 0.3 units
 Total Vol: 10 uL

Buffer:

MgCl₂: 1.5mM
 KCl: 50mM
 Tris: 100mM
 pH: 8.3

FEATURES Prepared with primer pairs derived from X04500.

source Location/Qualifiers

1..614
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

STS
 position: 180..408
 complement (389..408)

BASE COUNT 174 a 136 c 120 g 184 t

ORIGIN

Query Match 99.3%; Score 234.4; DB 11; Length 614;
 Best Local Similarity 99.6%; Pred. No. 3,40-37;
 Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 TTTGATTCATTCGCTAATTAATTAAGGGGCAAGAGTACAGTCTCTGTAAGAA 60
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 Db 671 TTTGATTCATTCGCTAATTAATTAAGGGGCAAGAGTACAGTCTCTGTAAGAA 430
 UY 61 GCTTATCTTTTAAATAGTATGATCAATTCGAGTGGTGTCTCTCTTAAATC 120
 |||||||
 Db 431 GCTTATCTTTTAAATAGTATGATCAATTCGAGTGGTGTCTCTCTTAAATC 490
 UY 121 AAGTCTTTAATTAATCAAGAAATATATAGTTCAGATTATTAATGCAATATTAA 180
 |||||||
 Db 491 AAGTCTTTAATTAATCAAGAAATATATAGTTCAGATTATTAATGCAATATTAA 550
 UY 181 AATATAGCAAAATATGATCAATTCGAGTGGTGTCTCTCTTAAATC 236
 |||||||
 Db 551 AATATAGCAAAATATGATCAATTCGAGTGGTGTCTCTCTTAAATC 606

RESULT 2

AX052806 9721 bp UNA linear PAT 12 JAN 2001
 DEFINITION Sequence 16 from Patient W0071753.
 ACCESSION AX052806
 VERSION AX052806.1 GI:12226963
 KEYWORDS

SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
 1 (bases 1 to 9721)

REFERENCE Korfman, R.S., Bull, G.W., Crossman, D.C., Francis, S.E. and
 Stephenson, K.
TITLE Diagnostics and Therapeutics for osteoarthritis
JOURNAL Patent: WO 0071753 A1 30-NOV-2000;
 Interleukin Genetics, Inc. (US)

FEATURES

source

1..9721
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 2661 a 2328 c 2122 g 2608 t 2 others
 The sequence may be

Query Match 99.3%; Score 234.4; DB 6; Length 9721;
 Best Local Similarity 99.6%; Pred. No. 1,60-47;
 Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 TTTGATTCATTCGCTAATTAATTAAGGGGCAAGAGTACAGTCTCTGTAAGAA 60
 |||||||
 Db 8710 TTTGATTCATTCGCTAATTAATTAAGGGGCAAGAGTACAGTCTCTGTAAGAA 8769
 UY 61 GCTTATCTTTTAAATAGTATGATCAATTCGAGTGGTGTCTCTCTTAAATC 120
 |||||||
 Db 8770 GCTTATCTTTTAAATAGTATGATCAATTCGAGTGGTGTCTCTCTTAAATC 8829
 UY 121 AAGTCTTTAATTAATCAAGAAATATATAGTTCAGATTATTAATGCAATATTAA 180
 |||||||
 Db 8840 AAGTCTTTAATTAATCAAGAAATATATAGTTCAGATTATTAATGCAATATTAA 8889
 UY 181 AATATAGCAAAATATGATCAATTCGAGTGGTGTCTCTCTTAAATC 236
 |||||||
 Db 8890 AATATAGCAAAATATGATCAATTCGAGTGGTGTCTCTCTTAAATC 8945

RESULT 4
 AX067266 9721 bp UNA linear PAT 24 JAN 2001
 DEFINITION Sequence 2 from Patient W0100880.
 ACCESSION AX067266
 VERSION AX067266.1 GI:12544890
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
 1 (bases 1 to 9721)

REFERENCE Bull, G.W., Cox, A., Camp, N.J. and di Giovanni, E.S.
TITLE Diagnostics and Therapeutics for diseases associated with an IL-1
 inflammatory haplotype
JOURNAL Patent: WO 0100880 A2 04 JAN 2001;
 Interleukin Genetics, Inc. (US)

FEATURES

source

1..9721
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 2661 a 2328 c 2122 g 2608 t 2 others

Query Match 99.3%; Score 234.4; DB 6; Length 9721;
 Best Local Similarity 99.6%; Pred. No. 1,60-47;
 Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 TTTGATTCATTCGCTAATTAATTAAGGGGCAAGAGTACAGTCTCTGTAAGAA 60
 |||||||
 Db 8710 TTTGATTCATTCGCTAATTAATTAAGGGGCAAGAGTACAGTCTCTGTAAGAA 8769
 UY 61 GCTTATCTTTTAAATAGTATGATCAATTCGAGTGGTGTCTCTCTTAAATC 120

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|||||
Db 8770 GGCAGTTTAAAGCATGATCATTCATTCAGTTGGACTGCTGCTCTTAAATC 8829
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QY 121 AAGTCCTTTAATTAAGCTGAAAAATATATAGTCAGATTATTAAATGGCAATTTAT 180
|||||
Db 8830 AAGTCCTTTAATTAAGCTGAAAAATATATAGTCAGATTATTAAATGGCAATTTAT 8889
|||
QY 181 AATGAGCAATATGAGTCTTCATGCTTGCAGAAATACCTGCATGAGAAAA 236
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Db 8890 AATGAGCAATATGAGTCTTCATGCTTGCAGAAATACCTGCATGAGAAAA 8945
|||||

RESULT 4
AX469435 9721 bp DNA linear PAT 16-JUL-2002
LOCUS AX469435
DEFINITION Sequence 1 from Patent WO222877.
ACCESSION AX469435
VERSION AX469435.1 GI:21901721
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hill,J.A., Wang,Z.C., Anderson,D.J. and Yunis,F.J.
TITLE Variants of IL-1 beta gene and ccd46 gene for diagnosing unexplained
JOURNAL recurrent pregnancy loss
PATENT: WO 022877-A 1 21-MAR-2002.
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) : DNA-FARHER CANCER
INSTITUTE, INC. (US)
FEATURES
Source 1.9721
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2661 a 2328 c 2122 g 2608 t 2 others
ORIGIN

Query Match 99.3%; Score 234.4; DB 6; Length 9721;
Best Local Similarity 99.6%; Pred. No. 1.6e-37;
Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCATTCATGCTGCTAATTTATTCAGAGGGGCAAGAGTACGACGTGCTGTAAAGA 60
|||||
Db 8710 TTTCATTCATGCTGCTAATTTATTCAGAGGGGCAAGAGTACGCTGTCTAAAGA 8769
|||||
QY 61 GCGTACTTTTAATAGCTATGCAATCAATTTGGAGCTGTGCTCTTTTAATC 120
|||||
Db 8770 GCGTACTTTTAATAGCTATGCAATCAATTTGGAGCTGTGCTCTTTTAATC 8829
|||||
QY 121 AAGCTCTTATTAAAGCTGAAAAATATATAGCTGAGATTATTAAATGGCAATTTAT 180
|||||
Db 8830 AAGCTCTTATTAAAGCTGAAAAATATATAGCTGAGATTATTAAATGGCAATTTAT 8889
|||||
QY 181 AATGAGCAATATGAGTCTTCATGCTTGCAGAAATACCTGCATGAGAAAA 236
|||||
Db 8890 AATGAGCAATATGAGTCTTCATGCTTGCAGAAATACCTGCATGAGAAAA 8945
|||||

RESULT 5
HSL11B 9721 bp DNA linear PRI 26-JUN-1997
LOCUS HSL11B
DEFINITION Human gene for prointerleukin 1 beta.
ACCESSION X04500
VERSION X04500.1 GI:33788
KEYWORDS Interleukin 1 beta.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 9721)
AUTHORS Clark,B.D., Collins,K.L., Gandy,M.S., Webb,A.C. and Auron,P.E.
TITLE Genomic sequence for human prointerleukin 1 beta: possible
evolution from a reverse transcribed prointerleukin 1 alpha gene

```

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JOURNAL Nucleic Acids Res. 14 (20), 7897-7914 (1986)
MEDLINE 87640762
PUBMED 3490654
COMMENT Data kindly reviewed (13-MAY-1988) by Clark B.D.
FEATURES
Source 1.9721
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="q13-q24"
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/feature="Alu repeat"
669..960
/misc_feature 1576..1581
/note="TATA-box like sequence"
1809..1816
CAAT_signal 1859..1866
TATA_signal 1903..1909
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exon 1934..2005
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2006..2465
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2458..2465
/misc_feature 1/note="pol. viral enhancer core sequence"
2466..2527
exon 1/number=2
cds 1010(2481..2527,3092..4143,5125..5426,5874..6038,
7275..7405,8127..8339)
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DGGILRLSDHRYSKGFRQASVYVAMDKLRKMLVPCDPTFOENDLSIFPEFIEEP
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SFVQGRHSNDKIPVALGKERNLYISCLKDKDKPTLQLESDFPNRYPKKKKEKRVN
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3144..5124
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4266..4273
/note="pol. viral enhancer core sequence"
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exon 1/number=4
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intron 1/number=4
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intron 1/number=5
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repeat_unit 1/note="Inverted repeat A"

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exon	<924..-970 /gene-"TLLB" /note "interleukin-1 beta; 600-120-094" CDS 120 094" /number 2 971..-1535 /gene-"TLLB" /note "TLLB Intron B: 600-120-094" 1536..-1587 /gene-"TLLB" /note "interleukin-1 beta; 600-120-094" /number 3 1588..-3575 /gene-"TLLB" /note "TLLB Intron C: 600-120-094" 3576..-3629 /note-"Alu repeat copy A: 600-120-094" 3576..-4777 /gene-"TLLB" /note "interleukin-1 beta; 600-120-094" /number 4 3778..-4822 /gene-"TLLB" /note "TLLB Intron D: 600-120-094" 4823..-4487 /gene-"TLLB"
Intron	/note "interleukin-1 beta; 600-120-094" /number 5 4488..-5722 /gene-"TLLB" /note "TLLB Intron E: 600-120-094" 5723..-5854 /gene-"TLLB"
exon	/note "interleukin-1 beta; 600-120-094" /number 6 5854..-6569 /gene-"TLLB" /note "TLLB Intron F: 600-120-094" 6570..-66782 /gene-"TLLB"
Intron	/note-"interleukin 1 beta; 600-120-094" /number 7 7280..-7379 /note-"Alu repeat copy B: 600-120-094" 7280..-7379
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REGION	242 bp upstream of HindII sites chromosome: 2413-921.
query Match	98.2% Score 231.8; DB % Length 7624;
best Local Similarity	99.1% Ident. No. 5,740 Y/N
Matches 233; Conservative	0; Mismatches 2; Indels 0; Gaps 0;

QY	2	TTTATTCATGTCGTAATTTATTCGAAGGGGCGAGAGTACAGTGTCTGTTAAAGAG	61
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QY	62	CCGAGTTTAAATAGCTATGCAATTCATTCATTTGGACTGCTGCTCTCTTTAAATCA	121
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QY	122	AGTCTTTAAATAGCTGAAATATATATAGCTACATATTTAAATGGCAATATTATA	181
Db	7273	AGTCTTTAAATAGCTGAAATATATATAGCTACATATTTAAATGGCAATATTATA	7332
QY	182	AATGACCAAAATATGCTGTTCATGCTGTGAAATTAACCTCATGGAAGAAA	236
Db	7333	AATGACCAAAATATGCTGTTCATGCTGTGAAATTAACCTCATGGAAGAAA	7387
RESULT 7			
LOCUS	AY137079	17447 bp	DNA linear PRI 05-AUG-2002
DEFINITION	Homo sapiens interleukin 1, beta (IL1B) gene, complete cds.		
ACCESSION	AY137079		
VERSION	AY137079.1	GI:22122009	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Okuyama, M.; Metzger, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	Rieder, M.J., Armet, T.Z., Carrington, D.P., Ozuna, M., Kuldanek, S.A., Rajkumar, N.R., Toth, E.J., Yi, Q. and Nickerson, D.A.		
TITLE	Direct Submission		
JOURNAL	Submitted (29-JUL-2002) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA		
COMMENT	to cite this work please use: SeattleSNPs, NHLBI HL66682 Program for Genomic Applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).		
FEATURES	Location/Qualifiers		
Source	1..17447		
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	/replace="q"		
	500..503		
variation	/frequency="0.96"		
	/replace="a"		
	794		
	/frequency="0.40"		
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variation	/frequency="0.01"		
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[illegible]

RESULT	B
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DEFINITION	AC079753 Homo sapiens BAC clone RP11-67114 from 2, complete sequence.
ACCSSION	AC079753
KEYWORDS	AC079753.7 GI:14318495
SOURCE	HIT.
ORGANISM	Homo sapiens. Homo sapiens Eukaryote; Metazoa; Chordata; Eumetazoa; Vertebrata; Euarchontomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; HOMO.
REFERENCE	1 (cases 1 to 154214) Sullivan,J.E. and Waterston,R. Toward a complete human genome sequence. <i>Genome Res.</i> 8 (11), 1097-1108 (1998)
JOURNAL	99063792
TITLE	(cases 1 to 154214) Adams,S., Cotton,M., Dowbor,A. and Rosso,C. The sequence of Homo sapiens BAC clone RP11-67114 Unpublished (2001)
AUTHORS	Waterston,R.H. Direct Submission Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	4 (cases 1 to 154214) Waterston,R.H. Direct Submission Submitted (06-JUN-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
JOURNAL	5 (cases 1 to 154214) Waterston,R.H. Direct Submission Submitted (04-JUL-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	6 (cases 1 to 154214) Waterston,R. Direct Submission Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
JOURNAL	7 (cases 1 to 154214) Waterston,R. Direct Submission Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT	on Jan 6, 2001 This sequence version replaced at:14029079. ----- Genome Center

Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@wustl.wustl.edu
 Summary Statistics
 Center project name: H_NH00671.14

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
 The Rpl1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Calane, J.J. and de Jong, P.J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
 VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the right is Rpl1-725J3. Actual start of this clone is at base position 1 of Rpl1-67L14; actual end is at base position 154214 of Rpl1-67L14.

There are polymorphic base differences in the overlap between Rpl1-67L14 and Rpl1-725J3.

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report_location	/rpt_family=MER2_1.yco*
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SFVQGESENKIPVALGLKELNLSGVLDKDKPTIQLSEVDKKNPKKKMKREVEFN
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BASE COUNT      438 a      365 c      330 g      389 t
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Best Local Similarity 98.7%; Pred. No. 1,8e-36;
Matches 232; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 11
LOCUS      E00846      1507 bp      RNA      linear      PAT 29-SEP-1997
DEFINITION cDNA sequence for human IL-1.
ACCESSION   E00846
VERSION     E00846.1 GI:2169107
KEYWORDS    JP 1986119191-A/1.
SOURCE      unidentified.
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 1507)
AUTHORS    Filitzou, P.A., Chiyarusu, F.D., Andorlyu, S.U., Arekisanada, R.,
            Shierudon, P.U., Rili, G., and Rani, J.R.
            HUMAN IL-1C DNA HAVING BIOLOGICALLY ACTIVE HUMAN IL-1 PROTEIN CODE
            PATENT: JP 1986119191-A 1 06-JUN-1986;
            MASSACHUSETTS INST OF TECHNOLOGY, NEW INGRAND MEDICAL CENTER
            HOSUPITARUZI INC., TRUSTEES OBU TAPUTSU KARETSUJI, VERESUREI
            KARETSUJI
COMMENT     OS Human (Homo sapiens)
            IN JP 1986119191-A/1
            PD 06-JUN-1986
            PR 18-MAY-1985 JP 1985104978
            PR 18-MAY-1984 US 84 611669, 11-FEB-1985 US 85 700374 PI
            PHIRITSUPU II ABRON, CHIYARUSU EF DEINAKRO, PI ANDORIYUU SHIT
            UPHU
            PI AREKISANDAA RITSUCHI, SHIERUDON EMU UOROFU, RII GEBRUE, PI
            RANIT JEE ROOZENATISUAA
            PC C12N15/00,A61K39/395,C07K13/00,C12N1/00,C12N5/00,C12P21/02, PC
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            PC C12R1:19),(C12P21/02,C12R1:19);
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            CC hypothetical: No;
            CC anti-sense: No;
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DEFINITION Sequence 1 from Patent EP 0161901.
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VERSION     I07942.1 GI:589345
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 1507)
AUTHORS    Auron, P.E., Webb, A.C., Gehlke, L., Diarell, C.A., Rosewasser, L.J.,
            Rich, A., and Wolff, S.M.
            Human IL-1 cDNA sequences encoding biologically active human IL-1
            proteins
            Patent: EP 0161901-A2 1 21-NOV-1985;
            Location/Qualifiers
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Best Local Similarity 98.3%; Pred. No. 2.4e-36;
Matches 232; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1269 TTTTATTCATTGGCTAATTATTCAGAAAGGGGCGACAGTAGCAGTGTCTGTAAAG 1428
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PE 06-MAR-1997 JP 1495344919
 ER 14-MAR-1986 JP 86P 57888, 20 JUN 1986 JP 86P 145830, PR
 09-UL-1986 JP 86P 161184, 27-AUG-1986 JP 86P 200324 P1 NAKA

SANOKI, KANEDA MAYUMI, KIKUMOTO YOSHIKAZU, KO HIDEIMITSU, PI KAWAI
 KAZUYOSHI, TAKEKATA SEISUOKO, ISHII KIYOSHI, PI YANAGIHARA YASUO,
 PI HIRAI YOSHIKATSU
 PC C07K14/545,C07H21/04,C12N1/21,C12N5/10,C12N15/09, PC
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 PC (C12N1/21,C12R1:19),(C12P21/02,C12R1:19),(C12P21/02,C12R1:91);
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 CC topology: linear;
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 QY 61 GCGTAGTTTAAATAGCTAGTCAATTCATTTGGAGTGGTCTGCTGCTTTAATG 120
 DB 1207 GCGTAGTTTAAATAGCTAGTCAATTCATTTGGAGTGGTCTGCTGCTTTAATG 1266
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